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I. Methods for breeding high-protein cultivars of soybeans; II. Transfer of Phytophthora resistance in soybean [Glycine max (L.) Merr] by backcrossing

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I. METHODS FOR BREEDING HIGH-PROTEIN CULTIVARS OF SOYBEANS. II. TRANSFER OF PHYTOPHTHORA RESISTANCE IN SOYBEAN (GLYCINE MAX (L.) MERR.) BY BACKCROSSING

Iowa State University PH.D. 1986

I. Methods for breeding high-protein cultivars of soybeans.

II. Transfer of *Phytophthora* resistance in soybean [*Glycine max* (L.) Merr.] by backcrossing

by

Othello Batulan Capuno

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GENERAL INTRODUCTION

Two important aspects of soybean breeding were dealt with in this dissertation. Both studies were intended to enhance efficiency in the development of improved soybean cultivars.

One objective in soybean breeding programs is the development of cultivars with high protein content. The demand for soybeans high in protein percentage for human consumption is increasing, especially in the manufacture of tofu. One of the commonly-used cultivars in the U.S. with high protein content for tofu production is Vinton 81. One limitation of this cultivar is that it has lower yield potential than that of other available cultivars. The need to find an effective breeding method to develop soybean cultivars with high yield and comparable protein percentage to Vinton 81 is important. The objective of this study was to determine whether single-cross or backcross populations would offer the best opportunity to select for higher yield than that of Vinton 81 while maintaining its current level of protein percentage.

Another objective in many soybean breeding programs is the transfer of Phytophthora resistance into susceptible cultivars. With the exception of the study of Wilcox et al. (1971), no studies have been conducted to evaluate the efficiency of the backcross procedure in the transfer of Phytophthora resistance into susceptible cultivars. The main goals of this study were to determine the number of backcross generations required to transfer a major gene for Phytophthora resistance into a cultivar and obtain lines with the yield potential of

the recurrent parent, and to determine in what back cross generation a composite of visually similar lines could be made that would yield as much as the recurrent parent.

SECTION I. METHODS FOR BREEDING HIGH-PROTEIN CULTIVARS OF SOYBEAN

INTRODUCTION

The protein percentage in the seed of currently-grown soybean cultivars in the U.S. is approximately 40.5% on a dry-weight basis (Hartwig, 1979). This protein percentage is far below the maximum value of 53% available in plant introductions that are part of the U. S. collection. Protein percentage in soybean can be genetically manipulated as evidenced by the high-protein cultivars Provar, Protana, Vinton, and Vinton 81. Further, the mean heritability for protein percentage in published reports is 76%, which suggests that selection for this trait could be successful (Table 1).

High-protein soybean cultivars are desirable for human consumption, especially in the manufacture of tofu. Tofu is a wet cake obtained by adding calcium sulphate to heated soybean milk. It is composed of water, protein, oil, carbohydrates, and ash of varying compositions. Wang et al. (1983) found that soybean cultivars with high protein content produced tofu with a higher ratio of protein to oil than did cultivars with smaller amounts of protein. The original protein and oil content of the beans is a factor in tofu yield and in the final protein and oil content of the tofu (Smith et al., 1960). Some soybean cultivars with high protein content were released, but their seed yields were inferior to commonly-grown cultivars. Therefore, it is important to improve the yielding capacity of soybean cultivars with high protein content.

One of the most recent cultivars released with a high-protein percentage is Vinton 81. This cultivar was released as a large-seeded

specialty cultivar similar to Vinton but possesses an allele at the Rps_1 locus that provides resistance to races 1 to 3 and 6 to 9 of phytopthora rot. It originated from the BC_4F_2 generation of the cross L60-347-4-4G-2-B x Vinton [5]. L60-347-4-4G-2-B is an F_7 line selected by the Ohio Agricultural Research and Development Center from the cross Harosoy x Higan for its resistance to phytopthora rot. Vinton is a large seeded specialty cultivar with about 45% protein and 22 g/100 seeds. However, the yield of Vinton 81 is lower than that of other presently grown cultivars. A quick and efficient method is important in improving the yield potential of Vinton 81, while maintaining its current level of protein percentage.

This study was conducted using F_4 and BC_1F_3-derived lines from crosses between Vinton 81 and three high-yielding parents of different maturity groups. The objectives were 1) to determine which kind of method (single cross vs backcross) would offer the best opportunity to improve seed yield while retaining the level of protein of Vinton 81, and 2) to identify individual lines with higher yield and comparable protein percentage to Vinton 81.

Table 1. Summary of heritability for protein percentage in soybean as reported by several authors[a]

Authors		Crosses[b]	Heritability[c] Percent
Johnson et al. (1955)	1.	AA x AA	39
	2.	AA x AA	83
Thorne and Fehr (1970b)	3.	AA x UH	91
	4.	(AA x UH) x AM	91
Shannon et al. (1972)	5.	AM x AM	88
	6.	AA x AM	89
	7.	AA x AA	92
Shorter et al. (1976)	8.	AA x UA	60
	9.	AM x UA	58
	10.	AA x AM	54
Erickson et al. (1981)	11.	Composite of 4 *G. max* x G. soja crosses	78
Openshaw and Hadley (1984)	12.	UH x AH	90
	13.	AM x AM	75
Overall mean			76

[a]Adopted from Burton (1984).

[b]AH = adapted, high protein line (> 46%); AM = adapted, moderately high protein line (42-46%); AA = adapted, average protein line (≤ 42%); UH, UM, UA = as above, except that U = unadapted.

[c]Calculated based on entry-mean basis.

REVIEW OF LITERATURE

Prospects for Soybean Cultivars with High Yield and High Protein Percentage

In some areas of the world, the soybean and its products are used for human consumption as a source of protein. One of the popular protein products of soybean is tofu. Tofu is the gel-like precipitate obtained by adding calcium sulphate to heated soybean milk (Smith and Circle, 1972). Fresh commercial tofu is usually sold in the form of wet cake, which has a white or light yellow color and a bland taste. It has an approximate composition of 6 % protein, 3.5 % fat, 1.9 % carbohydrate, 0.6 % ash, and 88 % water (Standard Table of Food Composition, 1954). Tofu is consumed by cutting the cake into small pieces, and serving it fresh in soup, frying it in deep fat, or other means of preparation.

Tofu is a traditional food in the Orient and is also becoming popular in the West. In China and Southeast Asia, Watanabe (1978) reported that over one billion people are dependent on tofu as a major source of food protein. In Japan, it has been estimated that the consumption of soybean for food is a million tons per year (Ministry of Agriculture and Forestry, 1978). Tofu makes up 40 % of this total. Japan imported 81 % of the soybean seed used for food products. In Taiwan, tofu is also popular. According to a report by Chiang and Huang (1979), there are 1,410 tofu factories dispersed around Taiwan. The majority of tofu makers are small family-type operations that use batch type or semiautomatic processors to make tofu.

In North America, the number of non-oriental tofu producers rose from 0 to 1975 to 167 in 1981, according to data from the Soyfoods Center (Shurtleff, 1982). More than 11,000 tons of soybeans are being used annually in the manufacture of tofu in the U.S. The soybean cultivar Vinton was released specifically for food use because of its high-protein content and large seed (Bahrenfus and Fehr, 1980). An improved cultivar, Vinton 81, was released in 1984, which has similar characteristics to Vinton, except that it possesses an allele at the Rps_1 locus that provides resistance to races 1 to 3 and 6 to 9 of phytopthora rot to which Vinton is susceptible (Fehr et al., 1984).

One of the major drawbacks of Vinton and Vinton 81 is that both had lower yields than that of other available cultivars. The development of high-protein cultivars with comparable yields to commonly grown cultivars would be important. It seems that productive soybean cultivars with high protein content would have some demand, both domestically and internationally.

Methods Used for Yield and Protein Improvement in Soybean

Several different methods have been used to develop high-yielding, high-protein soybean cultivars. Some success in combining yield and protein has been reported (Hartwig and Hinson, 1972; Brim and Burton, 1979). In most of these studies, however, their main goals either were to increase yield and protein percentage simultaneously or protein improvement only. None of the studies reported were aimed at increasing yield, while maintaining the protein percentage at a specified level as was done in my study.

Shannon et al. (1972) evaluated 78 F_2-derived lines in the F_4 generation from each of six soybean populations to determine which population had the best opportunity for improving yield, protein and the combination of yield and protein. The six populations tested included one cross of high yield x high yield parents, four high yield x high protein crosses and one high protein x high protein cross. These populations were derived from diallel crosses among two adapted high-yielding parents (Y_1 and Y_2) and two adapted high-protein parents (P_1 and P_2). The cross of P_1 x P_2 produced more lines high in protein percentage and in protein per hectare, and more lines that combined high yield with high protein. They also showed that the greatest genetic advances for yield and protein per hectare, was exceeded only by P_1Y_2 for predicted progress in protein percentage and was the only population in which expected genetic advance exceeded parental mean for percent protein and protein per hectare. However, its highest yielding lines were below the highest yielding lines in other populations as in P_1Y_1 and P_2Y_2.

The use of exotic (plant introduction) germplasm has been examined as a means of improving yield and protein (Thorne and Fehr, 1970a,b). The populations they studied were two-way crosses (adapted x exotic) and three-way crosses (adapted x exotic) x adapted parents. They found that the three-way crosses were more fruitful sources of superior lines than the two-way crosses. The high protein content of the plant introduction was readily transmitted to their progeny; and selection for productive high-protein lines from crosses involving plant introductions was

possible.

A wild-type soybean (Glycine ussuriensis Regel and Maack) from the Nanking River Valley had been used as a non-recurrent parent in a backcrossing program (Hartwig, 1969). Many lines from the third backcross with Lee used as the recurrent parent produced equal seed yield to the recurrent parent, an increase in protein of 10 to 15 %, and decline in oil.

In a discussion of methods for breeding for protein and yield, Brim and Burton (1979) suggested tandem recurrent selection, wherein cycles of selection for protein are followed by cycles of selection for yield. Sebern and Lambert (1984) used a type of tandem selection and found some success in identifying high, intermediate, and low percentage protein groups in the F_2 or F_3 generations, followed by selection for yield within the group in later generations. Other workers have referred to tandem selection in a more conventional backcross program wherein selection for protein is followed by selection for yield as high protein genes are crossed back into high-yielding germplasm. Erickson et al. (1981) mentioned that in breeding programs attempting to combine high yield and high protein content in soybeans, early generation selection for high protein content would be desirable.

Studies Designed for Protein Improvement in Soybean

Although the following studies have no direct relationship to my study, they are mentioned because their goals were more efficient improvement in protein percentage of soybean cultivars.

Openshaw and Hadley (1984) investigated the effectiveness of

selection based on selection indexes to modify the protein percentage of soybean seeds. Indexes designed to maximize protein percentage using the percentage of oil and sugar were not superior to direct selection for protein. The observed gain (0.3 %) in protein resulting from selection for oil and protein was far below the predicted gain (1.4 %). It seemed that slow progress will be achieved using methods designed to increase both protein and oil. The index methods were found to be more effective than selection for protein, followed by culling for oil percentage at the mean of the population.

Shorter et al. (1976) measured the relative selection efficiency of indirect selection compared with direct selection for protein and oil. Indirect selection for higher chemical yield per hectare through selection for higher seed yield was found as efficient as direct selection for higher chemical yield. A selection index that combined seed yield and either protein or protein plus oil percentage was no more efficient than direct selection for the corresponding chemical yield trait. Direct selection for chemical yield traits was more efficient than indirect selection for chemical yield via chemical percentage traits.

Early-generation mass selection without recombination was employed to increase protein in a composite population of F_2 plants from four *G. max* x *G. soja* crosses (Erickson et al., 1981). Mean protein content of each selected population was greater than the mean for the unselected control population (45.3 %). Mean protein increased from 45.3 % (control population) to 48.0 % using mass selection among F_2 plants, followed by

mass selection among F_3 plants. By delaying mass selection until the F_3 generation, the mean protein increased from 45.3 to 48.8 %.

Recurrent selection has been used to improve protein percentage. Miller and Fehr (1979) tested the effectiveness of recurrent selection for protein percentage in soybean seed based on direct selection for high protein and indirect selection for low oil percentage. A population was formed by crossing 12 high-protein lines with high-yielding lines followed by three generations of intermating. The evaluation was based on a random sample of 100 S_1 lines from the cycle 0 population. After one cycle of recurrent selection, both methods were effective for increasing protein percentage. Direct selection for high protein resulted in almost twice as much improvement as did for indirect selection based on low oil. Protein percentage increased from 43.1 % in the cycle 0 population to 43.9 % in the cycle 1 population when selection was based on low oil and 44.6 % when selection was based for high protein. Brim and Burton (1979) evaluated the usefulness of recurrent selection for increased protein in soybean using two populations, each with two different effective population sizes. A cycle of selection was developed by crossing selected lines, testing S_1 lines from the crosses, and selecting those with the highest protein percentage as parents for the next cycle. Results showed significant improvement in protein percentage in soybean seeds using recurrent selection. Average increases per cycle over the means of the base populations were 0.7 % for population I and 1.3 % for population II. In population I, which originated from a cross between two adapted lines

with differing oil and protein percentage, this represented a change from 46.3 % to 48.4 %. In population II, which was genetically diverse, the mean changed from 42.8 % to 46.1 %.

MATERIALS AND METHODS

Single-cross and backcross populations were developed from matings between Vinton 81 and three high-yielding cultivars. Vinton 81 was chosen because it is the most widely-used cultivar for the manufacture of tofu in the United States. Its preferred characteristics are seed with a yellow hilum, high protein, and large size. Hardin, Pride B216 and Cumberland were chosen because of their desirable yield and agronomic characteristics. The three cultivars represent different maturity groups: Hardin, maturity group I; Pride B216, maturity group II; and Cumberland, maturity group III. The single crosses, Vinton 81 x Hardin, Vinton 81 x Pride B216 and Vinton 81 x Cumberland, were produced at Ames, Iowa in 1980. In the winter of 1981, the BC_1F_1 seed was produced in the greenhouse by backcrossing Vinton 81 to F_1 plants of the three crosses. F_2 seed was produced by natural selfing of the F_1 plants. F_3 and BC_1F_2 seed was obtained from F_2 and BC_1F_1 plants at the Isabela Substation, University of Puerto Rico in November 1981. In February 1982, F_4 and BC_1F_3 seed were obtained from F_3 and BC_1F_2 seed plants in Puerto Rico. In each generation of selfing, single-seed descent was used by harvesting two bulk samples of one seed per plant. In Ames 1982, the two 1-seed samples were planted separately for each of the F_4 and BC_1F_3 populations. Six-hundred seeds per sample were planted. At least one-hundred, but not more than 125 plants or similar maturity were harvested form each of the six populations.

In May 1983, the F_4 and BC_1F_3-derived lines were grown at the Agronomy Research Center and the Burkey farm near Ames. They were

planted in single-row plots 60 cm long with 1 m between plots. A randomized complete block design was employed with two replications at each location. The lines of each population were subdivided into 4 sets, each containing 110 entries with 17 entries from each of the 6 populations in every set. Each set also contained four check cultivars and Vinton 81. Vinton 81 was repeated four times per set. The entries were evaluated for seed yield, maturity, lodging score, plant height, seed weight, protein percentage and oil percentage. Based primarily on maturity, 32 lines from each generation of the three crosses were selected for additional testing in 1984.

In May 1984, a replicated test was planted. The experimental unit was a two-row unbordered plot 4.6 m long with 68 cm between rows of the same plot and 102 cm between rows of adjacent plots. For each of the three crosses, a randomized complete block design with two replications was used. Each set consisted of 70 entries: 32 entries from the F_4 and BC_1F_3, four check cultivars and two replicates of Vinton 81. Each set was evaluated at three locations. The Vinton 81 x Hardin cross was evaluated at Manson, Ames, and Marshalltown, the Vinton x Pride B216 cross at Ames, Marshalltown, and Stuart, and Vinton 81 x Cumberland cross at Ames, Stuart, and Ottumwa. The seeding rate was 270 seeds per plot.

The following data were collected in 1984.

1. Seed yield - collected on all plots and expressed as grams per square meter ($g\ m^{-2}$).
2. Maturity - recorded as days after August 31 when 95 to 100%

of the pods had turned brown. Data were obtained for all locations of the Vinton 81 x Pride B216 cross and for two of the three locations for the other two crosses.

3. Lodging - scored at maturity on a scale from 1 (all plants erect) to 5 (plants prostrate). The data were collected at all locations, except for the Vinton 81 x Hardin cross at Manson.

4. Plant height - measured at maturity as the distance from the soil surface to the terminal node. Plant height data were collected at all locations, except for the Vinton 81 x Hardin cross at Manson.

5. Seed weight - measured as grams per 200 random whole seeds. The original weights expressed as g/200 seeds were converted into mg/seed by multiplying each value by a factor of 5.

6. Protein percentage - expressed in percentage on a moisture-free basis.

7. Oil percentage - expressed in percentage on a moisture-free basis.

Protein and oil analyses were made with an infrared analyzer by the USDA Northern Regional Research Center, Peoria, Illinois. The test was made for each entry in every replication.

Analyses of variance using a randomized complete-block design were made for each trait and generation. The check cultivars were not

included in the analyses.

Data were analyzed for the individual locations and combined across locations. In the analyses, locations were considered a random effect, while generations were assumed to be a fixed effect. For maturity, lines were assumed to be a fixed effect because the plants from which they were derived were selected for this trait. For yield, lodging, plant height, seed weight, and protein and oil percentage, lines were considered a random effect because there was no selection employed for these traits.

For the analyses of data at individual locations, the following model was used.

$$Y_{ij} = u + R_i + L_j + e_{ij}$$

where

Y_{ij} = observed value for the j^{th} population in the i^{th} replication,

u = overall mean effect,

R_i = effect of the i^{th} replication, i = 1 to 2,

L_j = effect of the j^{th} line, j = 1 to 66,

e_{ij} = error associated with the ij^{th} observation.

The following model was used for the analyses of data combined across locations:

$$Y_{ijk} = u + E_i + R_{ij} + L_k + (ER)_{ij} + e_{ijk}$$

where

Y_{ijk} = observed value of the k^{th} line in the j^{th} replication in the i^{th} location,

u = overall mean effect,

E_i = effect of the i^{th} location, i = 1 to 3,

R_{ij} = effect of the j^{th} replication in the i^{th} location, j = 1 to 2,

L_k = effect of the k^{th} line, k = 1 to 66

e_{ijk} = error associated with the ijk^{th} observation.

For each analysis of variance, the mean squares due to lines were partitioned into two components: a) variation among lines within generations, and b) variation among generations. The mean squares due to lines within generations were subdivided into three components: a) among lines within BC_1F_3, b) among lines within the F_4, and c) within duplicates of Vinton 81.

For the analyses of data at individual locations, the significance of lines and related components were tested against the error mean square (Table 2). For the analyses of data combined across locations, the significance of lines was tested against the location x line mean square. The lines within generations and the generation components were tested against their respective location x line mean square (Table 3).

L.S.D. values were calculated for the seven traits with significant values in the analysis of variance for data at individual locations and combined across locations. For comparing means of individual lines of the BC_1F_3 generation from the means of individual lines derived from F_4 generation, the L.S.D. value was calculated using the equation L.S.D. = $t_{df,0.05} \sqrt{EMS\ (1/V_1 + 1/V_2)}$, where EMS = error mean square, V_1 = number of values used in computing line means in BC_1F_3 generation, and V_2 = number of values used in computing line means in F_4 generation.

For comparing means of individual lines from either the BC_1F_3 or F_4 generation to Vinton 81 means, the L.S.D. value was calculated using the equation L.S.D. = $t_{df,\ 0.05} \sqrt{EMS\ (1/V_n + 1/V_p)}$, where EMS = error mean square, V_n = number of values used in computing generation means, and V_p = number of values used in computing line recurrent parent means.

Table 2. From of the analysis of variance for data from the F_4 and BC_1F_3-derived lines and Vinton 81 at individual locations with fixed and random line effects

Sources of variation	df[a]	Expected mean squares	
		Lines fixed	Lines random
Replications (R)	r-1	$\sigma_e^2 + L\sigma_r^2$	$\sigma_e^2 + L\sigma_r^2$
Lines (L)	$\ell\ell$-1	$\sigma_e^2 + RL^2$	$o_e^2 + R\sigma_\ell^2$
L/Generation	(ℓ-g)	$\sigma_e^2(\ell/g) + R(L/G)^2$	$\sigma_e^2(\ell/g) + R\sigma^2{}_{\ell/g}$
L in BC_1F_3	(ℓ_1-1)	$\sigma_{e(1)}^2 + RL_1^2$	$\sigma_{e(1)}^2 + R\sigma_{\ell(1)}^2$
L in F_4	(ℓ_2-1)	$\sigma_{e(2)}^2 + RL_2^2$	$\sigma_{e(2)}^2 + R\sigma_{\ell(2)}^2$
Vinton 81	(ℓ_v-1)	$\sigma_{e(v)}^2 + RL_v^2$	$o_{e(v)}^2 + Ro_{\ell(v)}^2$
Generations (G)	(g-ℓ)	$\sigma_{e(g)}^2 + RG^2$	$\sigma_{e(g)}^2 + R\sigma_{(g)}^2$
Error	(r-1)(ℓ-1)	σ_e^2	σ_e^2

[a]R = replications, L = lines, and G = generations.

Table 3. Form of the analysis of variance for data from BC_1F_3-derived and F_4-derived lines and Vinton 81 combined across locations

Source of Variation	df[a]	Expected mean squares	
		Lines fixed	Lines random
Locations (E)	(e-1)	$\sigma^2_x + R\sigma^2_e$	$\sigma^2_x + R\sigma^2_e$
Replications/E	e(r-1)	σ^2_x	σ^2_x
Lines (L)	(l-1)	$\sigma^2_y + R\sigma^2_{le} + REL^2$	$\sigma^2_y + R\sigma^2_{le} + RE\sigma^2_l$
L/Generation(G)	(l-g)	$\sigma^2_{y(l/g)} + R\sigma^2_{(l/g)e} + RE(L/G)^2$	$\sigma^2_{y(l/g)} + R\sigma^2_{(l/g)e} + RE\sigma^2_{(l/g)}$
L in BC_1F_3	(l_1-1)	$\sigma^2_{y(1)} + R\sigma^2_{l(1)e} + REL^2_1$	$\sigma^2_{y(1)} + R\sigma^2_{l(1)e} + RE\sigma^2_{l(1)}$
L in F_4	(l_2-1)	$\sigma^2_{y(2)} + R\sigma^2_{l(2)e} + REL^2_2$	$\sigma^2_{y(2)} + R\sigma^2_{l(2)e} + RE\sigma^2_{l(2)}$
Vinton 81	(l_v-1)	$\sigma^2_{y(v)} + R\sigma^2_{l(v)e} + REL_v$	$\sigma^2_{y(v)} + R\sigma^2_{l(v)} + RE\sigma^2_{l(v)}$
Generation	(g-1)	$\sigma^2_{y(g)} + R\sigma^2_{ge} + REG^2$	$\sigma^2_{y(q)} + R\sigma^2_{ge} + REG^2$

E x L	(e-1)(1-1)	$\sigma_y^2 + R\sigma_{le}^2$	$\sigma_y^2 + R\sigma_{le}^2$
E x L/G	(e-1)(1-g)	$\sigma_{y(l/g)}^2 + R\sigma_{l/ge}^2$	$\sigma_{y(l/g)}^2 + R\sigma_{l/ge}^2$
E x L in BC_1F_3	(e-1)(l_1-1)	$\sigma_{y(1)}^2 + R\sigma_{l(1)e}^2$	$\sigma_{y(1)}^2 + R\sigma_{l(1)e}^2$
E x L in F_4	(e-1)(l_2-1)	$\sigma_{y(2)}^2 + R\sigma_{l(2)e}^2$	$\sigma_{y(2)}^2 + R\sigma_{l(2)e}^2$
E x L in Vinton	(e-1)(l_v-1)	$\sigma_{y(v)}^2 + R\sigma_{l(v)e}^2$	$\sigma_{y(v)}^2 + R\sigma_{l(v)e}^2$
E x G	(e-1)(g-1)	$\sigma_{y(g)}^2 + R\sigma_{ge}^2$	$\sigma_{y(g)}^2 + R\sigma_{ge}^2$
Error	e(r-1)(l-1)	σ_y^2	σ^2_y

[a]E = locations, R=replications, L=lines, and G=generations.

RESULTS

Analyses of variance for individual locations for the seven traits of the three crosses indicated mostly significant results (Tables 4 to 12). For the Vinton 81 x Hardin cross, there were significant differences among all lines and among the lines within generations for the seven traits, except for yield at Manson and Ames (Tables 4 to 6). The duplicate entries for Vinton 81 were not significantly different for any character at the three locations. No significant variation was observed among generations for yield at Ames and Marshalltown, but significant differences were observed at Manson. The mean values for yield observed at Ames and Marshalltown were relatively close, whereas at Manson the mean yield of the duplicate entries of Vinton 81 was substantially lower than the mean yield of either BC_1F_3-derived or F_4-derived lines (Tables A1 to A3). Significant differences among generations were detected for all other characters studied, except for plant height in Ames and Marshalltown.

For the Vinton 81 x Pride B216 cross, the analysis of variance indicated that there were significant differences at all locations among all lines and among lines within generations for yield, maturity, lodging, height, seed weight, protein, and oil, except for yield at Ames and oil percentage at Stuart. Significant differences among generations for yield were obtained at Stuart, but not at the other two locations. Significant differences among generations were obtained for maturity, plant height, lodging score, seed weight, protein and oil, except for plant height at Marshalltown and oil content at Stuart.

Table 4. Analysis of variance for four traits from the Vinton 81 x Hardin cross at Manson in 1984

Sources of variation	df	Mean Squares			
		Yield	Seed weight	Protein	Oil
Replications	1	4907**	175	1.3	6.7**
Lines (L)	65	459	578**	2.0**	0.8**
L/Generation	63	439	422**	1.7**	0.8**
L in BC_1F_3	31	548	380**	1.3*	0.6
L in F_4	31	340	477**	2.2**	1.0*
Vinton 81	1	101	33	0.2	0.3
Generation	2	1087*	5475**	11.3**	1.5*
Error	65	357	60	0.8	0.5
C.V.(%)		8.8	4.3	2.1	3.3

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 5. Analysis of variance for seven traits from the Vinton 81 x Hardin cross at Ames in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Replications	1	588	9*	0.0	31	0	6.8**	7.4**
Lines (L)	65	788	10**	0.6**	108**	636**	2.6**	0.9**
L/Generation	63	794	11**	0.6**	110**	493**	2.0**	0.8**
L in BC_1F_3	31	548	7**	0.2**	99**	620**	1.3**	0.7**
L in F_4	31	964	14**	0.9**	122**	377**	2.7**	1.0**
Vinton 81	1	3187	0	0.0	64	138	0.7	0.1
Generation	2	580	6*	2.5*	43	5159**	22.7**	3.1**
Error	65	877	2	0.1	38	50	0.4	0.2
C.V.(%)		11.9	13.7	16.9	6.8	4.5	1.6	2.0

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 6. Analysis of variance for seven traits from the Vinton 81 x Hardin cross at Marshalltown in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Replications	1	2360**	3	0.0	44	1813**	0.6	0.4
Lines (L)	65	829**	25**	1.1**	91**	899**	1.6**	0.8**
L/Generation	63	852**	25**	1.0**	93**	544**	1.4**	0.8**
L in BC_1F_3	31	905**	26**	0.9**	189**	657**	1.2**	0.7**
L in F_4	31	801**	26**	1.2**	69**	447**	1.6**	0.8**
Vinton 81	1	767	2	0.0	72	18	0.3	0.1
Generation	2	119	10*	1.6**	39	12106**	6.9**	2.3**
Error	65	164	2	0.1	37	115	0.3	0.3
C.V.(%)		5.2	16.3	13.2	6.4	6.2	1.4	2.6

* **Significant at the 0.05 and 0.01 probability levels, respectively.

Table 7. Analysis of variance for seven traits from the Vinton 81 x Pride B216 cross at Ames in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Replications	1	71808**	8*	3.3**	891**	1508**	9.6**	12.2**
Lines (L)	65	969	11**	0.4**	110**	477**	1.8**	0.5**
L/Generation	63	977	11**	0.4**	108**	333**	1.4**	0.5**
L in BC_1F_3	31	1094	9**	0.3	91**	189**	0.9**	0.4**
L in F_4	31	868	13**	0.5**	128**	488**	1.9**	0.5**
Vinton 81	1	694	0	0.2	12	53	0.3	0.6
Generation	2	722	8**	0.8**	163**	5006**	15.2**	1.8**
Error	65	706	2	0.1	19	70	0.4	0.2
C.V.(%)		9.9	14.4	18.8	4.8	5.2	1.6	2.0

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 8. Analysis of variance for seven traits from the Vinton 81 x Pride B216 cross at Marshalltown in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Replications	1	353	93.3**	6.0**	5	1508**	2.4**	2.5**
Lines (L)	65	926**	28.6**	0.5**	115**	551**	1.3**	0.4**
L/Generation	63	933**	28.0**	0.5**	117**	465**	0.9**	0.4**
L in BC_1F_3	31	629**	31**	0.5**	109**	243**	0.8**	0.3**
L in F_4	31	1265**	26**	0.5**	129**	701**	1.0**	0.5**
Parent	1	69	1	0.3	2	33	0.0	0.0
Generation	2	701	48**	0.4*	39	3234**	12.2**	1.2**
Error	65	340	3	0.1	33	40	0.3	0.2
C.V.(%)		6.7	12.6	14.0	6.1	3.3	1.2	2.4

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 9. Analysis of variance for seven traits from the Vinton 81 x Pride B216 cross at Stuart in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Replications	1	2575**	12**	0.2	151**	120*	0.0	1.1*
Lines (L)	65	395**	11**	0.4**	111**	405**	1.4**	0.3
L/Generation	63	392**	11**	0.4**	112**	301**	1.3*	0.3
L in BC_1F_3	31	391**	8**	0.3**	112**	183**	1.1*	0.3
L in F_4	31	406**	14**	0.4**	115**	429**	1.4*	0.3
Vinton 81	1	2.7	0	0.0	1	8	0.2	0.0
Generation	2	492*	23**	0.3*	94*	3666**	5.3**	0.5
Error	65	146	1	0.1	16	30	0.7	0.2
C V.(%)		5.2	10.4	14.0	4.3	3.2	2.1	2.2

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 10. Analysis of variance for seven traits from the Vinton 81 x Cumberland cross Ames in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Replications	1	145	8	1.2**	552**	400**	2.3*	1.8**
Lines (L)	65	1199**	37**	0.6**	114**	393**	2.6**	1.0**
L/Generation	63	1064	32**	0.5**	115**	353**	1.8**	0.9**
L in BC_1F_3	31	958	42**	0.5**	132**	390**	1.7**	0.9**
L in F_4	31	1173	23**	0.6**	102**	320**	1.9**	1.0**
Vinton 81	1	966	0	0.0	0	203	0.1	0.0
Generation	2	5462**	197**	1.8**	92*	1660**	27.2**	3.2**
Error	65	727	3	0.1	26	60	0.5	0.2
C.V.(%)		11.0	12.2	15.4	5.1	4.7	1.8	2.0

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 11. Analysis of variance for seven traits from the Vinton 81 x Cumberland cross at Stuart in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Replications	1	295	26**	36.5**	668**	0	3.4**	0.0
Lines (L)	65	378**	46**	0.3**	116**	453**	2.7**	0.9**
L/Generation	63	307**	39**	0.3**	118**	409**	1.9**	0.8**
L in BC_1F_3	31	306*	48**	0.3**	121**	489**	2.1**	0.8**
L in F_4	31	318**	31**	0.3**	117**	340**	1.7**	0.7**
Vinton 81	1	2	0	0.0	9	78	0.2	0.0
Generation	2	2610**	284**	0.6**	57	1825**	26.8**	6.4**
Error	65	134	3	0.1	21	25	0.3	0.1
C.V.(%)		5.0	12.0	14.3	4.8	2.8	1.4	1.7

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 12. Analysis of variance for seven traits from the Vinton 81 x Cumberland cross at Ottumwa in 1984

Sources of variation	df	Mean Squares					
		Yield	Lodging	Height	Seed weight	Protein	Oil
Replications	1	137	2.0**	6	335**	0.0	0.5
Lines (L)	65	3952**	1.1**	136**	534**	3.2**	0.6**
L/Generation	63	3870**	1.1**	135**	454**	2.7**	0.5**
L in BC_1F_3	31	5334**	0.7**	150**	548**	2.9**	0.6**
L in F_4	31	2516**	1.5**	125**	372**	2.5**	0.4**
Vinton 81	1	455	0.6	0	43	2.6	0.8
Generation	2	6546**	0.7*	138	3075**	20.0**	3.4**
Error	65	538	0.2	59	38	0.5	0.2
C.V.(%)		7.8	12.7	7.5	3.3	1.7	2.0

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

For the Vinton 81 x Cumberland cross, results from the analyses of variance at individual locations indicated significant differences among lines for yield, maturity, lodging, height, seed weight, protein and oil at all three locations. Highly significant differences among lines within generations were observed for all characters, except for yield at Ames. The duplicate entries of Vinton 81 did not show any significant differences at all three locations. Significant differences among generations were observed for all characters studied, except for plant height in Stuart and Ottumwa.

The combined analysis of variance across locations for Vinton 81 x Hardin cross indicated highly significant differences among locations for the seven traits (Table 13). Large deviations in mean values for the seven traits in the three locations were observed (Table C1). Highly significant differences among lines also were obtained for all the traits. This suggested that sufficient genetic variability existed among lines for the characters studied. No significant line x location interactions were obtained for yield, height, protein, and oil, but significant differences were observed for maturity, lodging score, and seed weight. There were significant lines within generation x location interactions. There were no location interactions observed for the duplicate entries of Vinton 81 for all traits.

The analysis of variance combined across locations for the Vinton 81 x Pride B216 cross revealed highly significant differences among locations for yield, maturity, lodging score, height, seed weight, protein and oil (Table 14). Mean for yield at Stuart were somewhat

Table 13. Analysis of variance for seven traits from the Vinton 81 x Hardin cross combined across locations in 1984

Sources of variation	df[b]	Mean Squares[a]						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Locations (E)	2 (1)	47496**	10*	53.6**	2269**	13560**	162.9**	82.5**
Rep/E	3 (2)	2619**	6*	0.0	37	663**	2.9**	4.9**
Lines (L)	65	900**	32**	1.2**	159**	1848**	4.9**	1.8**
L/Generation	63	917**	33**	1.2**	162**	1214**	3.9**	1.7**
L in BC_1F_3	31	887**	29**	0.8**	181**	1449**	2.8**	1.5**
L in F_4	31	881**	37**	1.6**	148**	1014**	5.0**	2.0**
Vinton 81	1	2957	1	0.0	0	158	1.0	0.4
Generations (G)	2	347	15**	3.8**	63	21800**	38.2**	6.6**
E x L	130 (65)	588	3**	0.4**	40	133**	0.6	0.3
E x L/G	126 (63)	584	3**	0.4**	41	122**	0.6	0.3

E x L in BC_1F_3	62 (31)	557	4**	0.4**	36	104**	0.5	0.3
E x L in F_4	62 (31)	612	3	0.5**	43	144**	0.7	0.4
E x Vinton 81	2 (1)	549	1	0.0	136	16	0.1	0.1
E x G	4 (2)	719	1	0.4*	18	474**	1.4*	0.2
Error	195 (130)	466	2.0	0.1	38	75	0.5	0.3
C.V.(%)		9.1	15.0	14.7	6.6	5.1	1.7	2.7

[a]Mean squares for maturity, lodging, and height were calculated based on two locations only.

[b]Numbers enclosed in parenthesis indicate the number of degrees of freedom for maturity, lodging, and height.

*,**Significant at the 0.05 and 0.01 probability levels, respectively.

Table 14. Analysis of variance for seven traits from the Vinton 81 x Pride B216 cross combined across locations in 1984

Sources of variation	df	Mean Squares						
		Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
Locations (E)	2	60564**	493**	22.9**	278**	33907**	140.5**	95.4**
Rep/E	3	24912**	38**	3.2**	349**	1045**	4.0**	5.3**
Lines (L)	65	1236**	44**	0.8**	280**	1276**	3.1**	0.6**
L/Generation	63	1228**	43**	0.8**	281**	943**	2.2**	0.6**
L in BC_1F_3	31	1121**	40**	0.8**	250**	478**	1.7**	0.3*
L in F_4	31	1362**	47**	0.9**	321**	1437**	2.8**	0.8**
Vinton 81	1	363	0	0.4	0	38	0.0	0.3
Generations (G)	2	1509*	69**	1.0**	248**	11768**	30.7**	3.1**
E x L	130	527*	4**	0.2**	28	78**	0.7**	0.3**
E x L/G	126	537*	4**	0.2**	28	78**	0.7**	0.3**

E x L in BC_1F_3	62	497	4**	0.2	31*	69*	0.6	0.4**
E x L in F_4	62	589*	3	0.2**	25	90**	0.8*	0.3
E x Vinton 81	2	201	1	0.0	8	28	0.2	0.1
E x G	4	203	5*	0.3*	24	75	1.0	0.2
Error	195	397	2	0.1	23	47	0.5	0.2
C.V.(%)		7.7	12.8	15.5	5.1	3.9	1.7	2.2

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

lower than at Ames and Marshalltown (Table C2). Mean protein percentage at Marshalltown was higher than the other two locations. Highly significant differences were observed among all lines and among lines within generations for the seven traits studied. For lines within the BC_1F_3 and F_4 generations, significant differences were found for all the traits. On the other hand, the duplicate entries of Vinton 81 did not show any significant differences. Highly significant differences among generations were observed for yield, maturity, lodging, height, seed weight, protein, and oil. The line x location and line within generation x location interactions were significant for all traits, except plant height.

The combined analysis of variance across three locations for the Vinton 81 x Cumberland cross revealed significant differences among locations for yield, lodging, height, seed weight, protein and oil, but not for maturity (Table 15). A wide variation for mean yield was obtained at the three locations, with Ottumwa producing the highest yield and Stuart the least. Mean protein percentage for Ames and Stuart were similar, whereas at Ottumwa, the mean protein percentage was higher than at the other two locations. Significant differences were found among lines and among lines within generations for the seven traits studied. The lines within the BC_1F_3 and F_4 generations were significantly different. The duplicate entries of Vinton 81 did not show any significant differences for all the traits. Significant differences were detected among the different generations for the seven traits studied. Significant line x location and line within generation

Table 15. Analysis of variance for seven traits from the Vinton 81 x Cumberland cross combined across locations in 1984

Sources of variation	df[b]	Mean Squares[a]						
		Yield	Maturity	Lodging	Seed Height	weight	Protein	Oil
Locations (E)	2 (1)	169531**	3	95.7**	732**	9536**	31.8**	21.1**
Rep/E	3 (2)	192	17**	13.2**	409**	246**	1.9**	0.8**
Lines (L)	65	2754**	79**	1.5**	255**	1261**	7.3**	2.0**
L/Generation	63	2437**	67**	1.5**	259**	1100**	5.2**	1.7**
L in BC_1F_3	31	3101**	84**	1.1**	281**	1313**	5.9**	1.8**
L in F_4	31	1852*	51**	1.8**	245**	919**	4.8**	1.6**
Vinton 81	1	24	0	0.2	3	90	1.0	0.4
Generations (G)	2	12736**	477**	1.9**	130*	6338**	72.9**	12.5**
E x L	130 (65)	1387**	4	0.3**	55**	59**	0.6*	0.3**
E x L/G	126 (63)	1402**	4	0.3**	55**	58**	0.6*	0.3**

E x L in BC_1F_3	62 (31)	1749**	5	0.2	61**	57*	0.4	0.2*
E x L in F_4	62 (31)	1077**	3	0.3**	49	57**	0.7	0.3**
E x Vinton 81	2 (1)	699	0	0.2	3	115	0.9	0.2
E x G	4 (2)	942	4	0.6**	79	110*	0.6	0.2
Error	195 (130)	466	3	0.2	35	40	0.4	0.2
C.V.(%)		8.4	12.1	14.1	6.0	3.7	1.6	1.9

[a]Mean squares for maturity were calculated based on data from two locations only.

[b]Numbers enclosed in parentheses indicate the number of degrees of freedom for maturity only.

*,**Significant at the 0.05 and 0.01 probability levels, respectively.

x location were obtained for all the traits except maturity. The line within generation x location interactions for lines derived from the BC_1F_3 generation were not significant for maturity, lodging, and protein and oil percentage. Significant differences were obtained for the lines within generation x location interaction for the F_4 generation for yield, lodging, seed weight and protein. The performance of Vinton 81 seemed to be consistent because no significant differences were observed between duplicate entries for the characters studied. For most traits, there was no location x generation interaction was found.

The coefficients of variation (CV) for each trait based on data combined across locations were slightly larger for the Vinton 81 x Hardin cross than the two other crosses (Tables 13 to 15). The highest CVs were for lodging score in the three crosses, ranging from 14.1 to 15.5 %. Protein percentage had the lowest CV, with a range from 1.6 to 1.7%. In general, the order of values from highest to lowest were lodging score > maturity > yield > height > seed weight > oil and protein. Similar trends were found for data collected from individual locations for the three soybean crosses.

The comparisons of the mean performance of seven traits across environments for the three soybean crosses revealed varied results (Tables 16 to 18). The BC_1F_3-derived lines of the Vinton 81 x Hardin cross did not differ significantly from F_4-derived lines for yield and plant height. The lines derived from BC_1F_3 generation exhibited significantly higher seed weight, higher protein percentage and lower oil than the lines derived from the F_4 generation. Vinton 81 had a

Table 16. Mean values for seven traits of BC_1F_3-derived and F_4-lines and Vinton 81 from the Vinton 81 x Hardin cross averaged across three locations in 1984

Generation and parent	Trait[a]						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	236	9.7	2.2	94	180	42.2	20.5
F_4	238	9.0	2.5	92	161	41.4	20.9
Vinton 81	236	9.6	1.8	95	200	42.4	20.4
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	ns[b]	0.4	0.1	ns	2	0.1	0.1
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	ns	1.0	0.2	ns	5	0.4	0.3

[a]Maturity, lodging and height were recorded only in two locations, hence, means were based from two locations only, instead of three.

[b]ns = The mean squares for differences among generations were not significant ($P > 0.05$), therefore, no L.S.D. value was computed.

Table 17. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Pride B216 cross averaged across three locations in 1984

Generation and parent	Trait[a]						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	256	10.5	2.1	94	182	41.6	21.1
F_4	261	11.3	2.2	92	168	40.9	21.3
Vinton 81	252	8.3	1.8	95	196	42.3	20.7
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	4	0.3	0.1	1	1	0.1	0.1
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	12	0.8	0.2	3	4	0.4	0.3

Table 18. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Cumberland cross averaged across three locations in 1984

Generation	Trait						
	Yield	Maturity[a]	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	252	13.6	2.7	100	180	41.2	20.9
F_4	266	16.5	2.8	99	169	40.0	21.4
Vinton 81	237	7.6	2.2	95	188	42.0	20.8
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	4	0.4	0.1	1	1	0.1	0.1
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	13	1.2	0.3	4	4	0.4	0.3

[a]Maturity was recorded at only two locations.

lower lodging score, higher seed weight, greater protein percentage and lower oil content than the bc_1F_3-derived and F_4-derived lines.

For the Vinton 81 x Pride B216 cross, the BC_1F_3-derived lines had significantly lower yield, earlier maturity, lower lodging scores, greater plant height, higher seed weight, higher protein percentage, and lower oil percentage than the F_4-derived lines (Table 17). Vinton 81 was significantly different from the BC_1F_3-derived and F_4-derived lines for maturity, lodging score, height, seed weight, protein percentage, and oil percentage. The BC_1F_3-derived and F_4-derived lines did not differ significantly from Vinton 81 for yield.

For the Vinton 81 x Cumberland cross, the means of the BC_1F_3-derived and F_4-derived lines were significantly different for all traits (Table 18). Vinton 81 differed significantly from the mean of BC_1F_3-derived lines in all traits, except for oil percentage. The F_4-derived lines differed significantly from Vinton 81 in all traits. Except for mean yield, both the BC_1F_3-derived and F_4-derived lines were different in most agronomic characters from Vinton 81. Lines derived from BC_1F_3 had significantly higher protein percentage and larger seed size than the F_4-derived lines. On the other hand, the F_4-derived lines showed higher mean yield and mean oil percentage than the BC_1F_3-derived lines. Vinton 81 showed the highest protein percentage, but its mean yield was significantly lower than the mean of the $BC1F_3$-derived lines. Vinton 81 showed the highest protein percentage, but its mean yield was significantly lower than the mean of the BC_1F_3-derived and F_4-derived lines.

The percentage of lines greater than, equal to, or worse than Vinton 81 was determined for the two most important traits, yield and protein percentage, averaged across locations (Table 19). Most of the lines derived from the BC_1F_3 generation of the Vinton 81 x Hardin cross had yields equal to Vinton 81. None of the individual lines of Vinton 81 x Hardin cross had yields superior to Vinton 81. For protein percentage, the BC_1F_3 generation had almost twice as many lines compared with the F_4 generation which had equal protein percentage with Vinton 81. Only a very small percentage of lines derived from the BC_1F_3 and F_4 generations had significantly higher protein percentage than Vinton 81.

For the Vinton 81 x Pride B216 cross, more F_4-derived lines than BC_1F_3-derived lines had a yield greater than Vinton 81 (Table 19). Twenty-five percent of the F_4-derived lines had a significantly higher yield than Vinton 81. On the other hand, only 9 % of the BC_1F_3-derived lines had higher yield than Vinton 81. No line of either generation significantly exceeded the protein percentage of Vinton 81.

For the Vinton 81 x Cumberland cross, a substantial percentage of lines had greater yields than Vinton 81. Seventy-two percent of the BC_1F_3-derived lines had significantly higher yields than Vinton 81, while only about 38 % of the F_4-derived lines had yields superior to Vinton 81. For protein percentage, 43 % of the lines of BC_1F_3 had equal or better protein percentage than Vinton 81. On the contrary, only 6 % of the F_4-derived lines had similar or better protein percentage than Vinton 81.

To identify lines with potential for release as cultivars, the

Table 19. Percentage of lines in each generation of each cross that are greater than, equal to, or worse than Vinton 81 for two traits for the three crosses averaged across three locations[a]

Cross	Generation	Performance	Yield (%)	Protein (%)
Vinton 81 x Hardin	BC_1F_3	Greater than	0	6
		Equal to	94	75
		Less than	6	19
	F_4	Greater than	3	3
		Equal to	91	34
		Less than	6	63
Vinton 81 x Pride B216	BC_1F_3	Greater than	9	0
		Equal to	88	50
		Less than	3	50
	F_4	Greater than	25	0
		Equal to	72	16
		Less than	3	84
Vinton 81 x Cumberland	BC_1F_3	Greater than	38	9
		Equal to	59	34
		Less than	3	56
	F_4	Greater than	72	3
		Equal to	28	3
		Less than	0	94

[a]Based on L.S.D. at 0.05 level of probability.

highest yielding lines from each generation of the three crosses with a protein percentage not significantly different from Vinton 81 were selected (Table 20). The highest yielding line of each generation was not necessarily represented because some of the highest yielding lines did not possess a protein percentage equal to Vinton 81. For the Vinton 81 x Hardin cross, the best line was obtained from BC_1F_3 generation. It had an 8.9 % greater yield and 2.6 % greater protein percentage than Vinton 81. For the other two crosses, the best lines for yield and protein were identified from the F_4 generation. A 13.1 % increase in yield and about 1 % increase in protein content were observed for the best line in the F_4 generation of the Vinton 81 x Pride B216 cross. In comparison, about a 6 % increase in yield was obtained with the best line from the BC_1F_3 generation. The best line in the F_4 generation of the Vinton 81 x Cumberland cross produced a yield increase of 14.3 % and a protein increase of 1.7 %.

Estimates of phenotypic and genotypic correlations for seed yield and protein percentage were calculated based on entry means (Table 21). Phenotypic correlations for seed yield and protein percentage of the BC_1F_3 generation for two of the three crosses were negative and non-significant. For the F_4 generation, the phenotypic correlation coefficients for the three crosses were all negative and were non-significant. Significant negative genotypic correlations for seed yield and protein percentage were observed in two out of three crosses of the BC_1F_3 generation. Also, negative estimates of genotypic correlation for yield and protein percentage were indicated in the F_4 generation in two

Table 20. Highest-yielding line for each generation selected for yield with no significantly different percent protein to the mean of two entries of Vinton 81 for the three crosses averaged across three locations

Cross	Generation or Parent	Trait		
		Yield ($g\ m^{-2}$)	Maturity (days)	Protein (%)
Vinton 81 x Hardin	BC_1F_3	257	15	42.9
	F_4	253	6	41.9
	Vinton 81	236	10	42.4
$L.S.D._{(0.05)}$		21	1.4	0.7
Vinton 81 x Pride B216	BC_1F_3	268	9	42.1
	F_4	285	11	42.7
	Vinton 81	252	8	42.3
$L.S.D._{(0.05)}$		20	1.4	0.7
Vinton 81 x Cumberland	BC_1F_3	251	15	41.7
	F_4	271	11	42.7
	Vinton 81	237	8	42.0
$L.S.D._{(0.05)}$		21	1.7	0.6

Table 21. Phenotypic and genotypic (in parentheses) correlations between yield and protein percentage for the BC_1F_3-derived and F_4-derived lines of three soybean crosses for 1984

Generation	Cross		
	Vinton 81 x Hardin	Vinton 81 x Pride B216	Vinton 81 x Cumberland
BC_1F_3	0.08	- 0.44	- 0.63*
	(0.16)	(-0.63)*	(-0.90)*
F_4	- 0.23	- 0.04	- 0.21
	(- 0.43)	0.01	- 0.20

*Significant at the 0.05 level of probability.

of three crosses studied, although they were all non-significant. In general, the coefficients for the genotypic correlations were larger than for the phenotypic correlations.

All estimates of genetic variance for yield in the three crosses, except for the BC_1F_3 generation in the Vinton 81 x Pride B216 cross, did not exceed twice their respective standard errors and were considered not statistically different from zero (Table 22). The estimates for the other six traits, except for oil percentage of the BC_1F_3 generation from Vinton 81 x Pride B216 cross, exceeded twice their respective standard errors and were judged statistically different from zero. The genetic variance estimates between any two generations for a certain character were considered significantly different if the difference between their variances was more than the sum of their standard errors of their estimates. For Vinton 81 x Hardin cross, the estimates of the genetic variances for the two generations were non-significant for all traits, except for lodging score. Higher genetic variance for lodging scores was obtained in the F_4 generation than the BC_1F_3 generation, and higher mean values for lodging score were observed in the F_4 generation compared with the BC_1F_3 generation (Table 16). For the Vinton 81 x Pride B216 cross, the estimates of genetic variance for yield, maturity, lodging score, plant height, and protein percentage between the BC_1F_3 and F_4 generation were not significantly different. Only seed weight and oil percentage had estimates of genetic variances that were significantly different between the two generations. For the Vinton 81 x Cumberland cross, no significant differences were detected in the

Table 22. Estimates of genetic variances (σ^2_g) and their standard errors for seven traits measured on BC_1F_3-derived and F_4-derived lines from three soybean crosses in 1984

Vinton 81 x Hardin

Trait	BC_1F_3	F_4
Yield	55.0 ± 40.0	45.0 ± 40.0
Maturity	6.1 ± 1.8	8.5 ± 2.3
Lodging	0.11 ± 0.05	0.28 ± 0.10
Height	36.2 ± 11.3	26.2 ± 9.5
Seed weight	224.0 ± 60.0	146.0 ± 42.5
Protein	0.38 ± 0.12	0.71 ± 0.21
Oil	0.20 ± 0.06	0.26 ± 0.08

Vinton 81 x Pride B216

Trait	BC_1F_3	F_4
Yield	104.0 ± 48.0	129.0 ± 59.0
Maturity	6.0 ± 1.7	7.3 ± 1.9
Lodging	0.10 ± 0.03	0.12 ± 0.04
Height	36.5 ± 10.3	49.3 ± 13.2
Seed weight	68.0 ± 20.0	224.0 ± 47.5
Protein	0.18 ± 0.07	0.33 ± 0.12
Oil	-0.01 ± 0.02	0.08 ± 0.03

Table 22. (continued)

Trait	Vinton 81 x Cumberland	
	BC_1F_3	F_4
Yield	225.0 ± 137.0	129.0 ± 82.0
Maturity	19.8 ± 5.2	12.0 ± 3.1
Lodging	0.15 ± 0.05	0.25 ± 0.08
Height	36.6 ± 11.7	32.7 ± 10.2
Seed weight	209.0 ± 50.0	144.0 ± 38.0
Protein	0.90 ± 0.24	0.68 ± 0.20
Oil	0.26 ± 0.08	0.21 ± 0.06

estimates of genetic variances for the seven traits between the F_4 and BC_1F_3 generation.

DISCUSSION

In breeding high-protein cultivars, there is emphasis on high protein content and high yield. Simultaneous improvement for the two characters seems to be slow because of the negative correlation that exists between them. For cultivars to be commercially acceptable, they must be equal in productivity to presently-grown cultivars and have a high protein content. My study seeks to know which of two methods, the single cross or the backcross, would be effective to develop soybean cultivars with higher yield than Vinton 81 while maintaining its protein content. Results revealed significant differences among lines for all traits evaluated. Significant yield improvement compared with Vinton 81 were observed in either type of cross for two of the three maturity classes. On the other hand, the mean protein percentage of both methods in the three crosses (except BC_1F_3 of Vinton 81 x Hardin cross) were significantly lower than Vinton 81. The single-cross and the backcross method differed in direction in yield and protein improvement. The single-cross method in improving seed yields, while the latter was more successful than the former in protein improvement.

The unique aspect of my research is that it will help plant breeders which method to use in developing cultivars that are higher yielding and have comparable protein percentage to Vinton 81. A method that is more effective than another will provide greater efficiency in planning and designing of breeding programs for developing cultivars that yield more than Vinton 81, but with similar protein percentage.

The majority of lines from the BC_1F_3 and F_4 generations produced

equal or better yields than Vinton 81 (Table 19). On the average, the percentage of lines with yield superior to Vinton 81 were 17 % for the Vinton 81 x Pride B216 cross and 55 % for the Vinton 81 x Cumberland cross. No marked improvement protein percentage based on individual line performance was observed. Only a very small percentage of the lines had significantly higher protein content than Vinton 81. In fact, a substantial number have significantly lower protein content than Vinton 81. This result closely agrees with the finding of Cianzio and Fehr (1982) who reported that no line equalled or exceeded the better parent in protein content in crosses between the low protein cultivars Wells and Woodworth and the high protein cultivar PI 153269. In the three crosses of my study, the BC_1F_3 population consistently produced higher percentage of lines with higher or equal protein percentage than the recurrent parent compared to the F_4 population.

The best lines for yield and protein in comparison with the mean of Vinton 81 were obtained from the F_4 population in two of the three crosses. These two lines (A84-474044 and A84-475049) were considered exceptional because only one line from the F_4 generation of each cross mentioned was found. The possibility that these two lines identified were merely due to chance cannot be ruled out because majority of the lines did not have this combination. The findings from this study are not conclusive for determining which approach is best for the development of soybean cultivars with high yield and high protein percentage. The results indicate the possibility of improving soybean yield and protein by either method. This is supported by the fact that

some individual lines from both types of crosses showed improvement in seed yield, while still maintaining the level of protein content of Vinton 81.

Phenotypic and genotypic correlations for seed yield and protein varied among crosses. For Vinton 81 x Hardin cross, there was no significant association between seed yield and protein content which suggested that selection for high yield, high protein lines would not be difficult for both generations. However, no lines from this cross significantly exceeded Vinton 81 in yield while retaining high protein content. In the Vinton 81 x Pride B216 cross, a significant negative genotypic correlation between seed yield and protein percentage was observed only in the BC_1F_3 generation. The high value of -0.63 in this generation could create a problem in identifying lines with high yield and protein content. This is not true, for the F_4 generation, however, because a positive correlation was found, which suggested that selection of lines high in yield and protein percentage (42.7). This is evidenced by data shown in Table 20, wherein line A84-474044 showed high yield (285 g m^{-2}) and high protein percentage. This result is in accordance with the theoretical expectation of Hanson et al. (1961) and Shimura and Hanson (1970) who concluded that the genetic correlation between protein percentage and seed yield was small and positive, so that high yield-high protein combinations should be possible if nitrogen was not limiting or other physiological restrictions were not present. On the other hand, negative correlations for seed yield and protein percentage were shown for both generations of Vinton 81 x Cumberland cross. The

high negative correlation values may create some difficulty in the selection of lines with high seed yield and high protein content. Negative correlation between seed yield and protein percentage were reported by several authors (Blixt, 1979; Gottschalk and Mueller, 1982; Hartwig, 1979; Kaul, 1982; Kwon and Torrie, 1964; Pandey et al., 1979; Shannon et al., 1972; and Thorne and Fehr, 1970a).

The estimates of genetic variance for both generation did not show significant differences for yield except between the BC_1F_3 and F_4 generation of Vinton 81 x Cumberland cross. The genetic variance in the BC_1F_3 was much higher than the genetic variance of the F_4 generation. This may be attributed to a wider range of values observed for this generation (Table B3). The estimates of genetic variances for protein of the F_4 generation were slightly higher than the BC_1F_3 generation in two of the three crosses.

It was demonstrated from my study that neither of the two methods employed was convincingly superior over the other for developing cultivars with high protein content. On the basis of performance of individual lines, two potential lines with significantly better yield and equal protein percentage with Vinton 81 were identified. This lead to me to believe that the single-cross method would be more appropriate method to use than the backcross in the development of cultivars with more yield than Vinton 81 and with the protein percentage of the latter. It is worthwhile to mention that three of the four cultivars with high protein content released from 1961 up to the present time originated from single crosses of homozygous parents. On the other hand, only

Vinton 81 was developed through the backcross procedure. Another reason for its choice is the simplicity of the single-cross method compared with the backcross because it requires less artificial hybridization. The method usually involves selection of a high yielding non-recurrent parent and a high protein parent. A single cross will be made between the two selected parents. The F_1 produced would be allowed to self naturally to obtain seeds of the F_2 generation. Lines derived from this generation will produce seed of F_3 and F_4 generation using the same procedure as in the development of F_2 generation. Lines derived from the F_4 generation will be evaluated to select lines with higher yield and similar protein percentage to the high protein parent.

SUMMARY AND CONCLUSION

The single cross and the backcross methods were evaluated to determine which method is more effective in the development of cultivar with higher yield and comparable protein percentage to Vinton 81. Hardin, Pride B216, and Cumberland were crossed to Vinton 81, a moderately high protein cultivar. Lines derived from the F_4 and BC_1F_3 generations were developed. BC_1F_3 lines were generated by backcrossing the F_1 hybrids to Vinton 81. Lines were selected from each generation based primarily on maturity. These lines were evaluated for yield, maturity, lodging, height, seed weight, protein, and oil at three locations in 1984. A duplicate entry of Vinton 81 was included in the evaluation for each of the cross.

Significant differences among lines were observed for all traits evaluated. Yield improvement was indicated in two of the three crosses. On the average, 17 % of the lines of Vinton 81 x Pride B216 and 55% of the lines of Vinton 81 x Cumberland cross yielded more than Vinton 81. For protein percentage, only 4.5 % of the lines Vinton 81 x Hardin cross and 6 % of the lines from Vinton 81 x Cumberland cross significantly exceeded Vinton 81.

The single cross and backcross methods were not markedly different for generating lines with better yield and equal protein percentage compared with Vinton 81. The two lines that were significantly superior for yield and protein came from the F_4-generation. Negative and positive correlation values between seed yield and protein percentage were observed. Comparisons of the estimates of genetic variances for

the F_4-derived and BC_1F_3-derived lines were all non-significant, except for lodging score.

The single-cross method is recommended over the backcross method in the development of soybean cultivars with increased yield and similar protein percentage to current high-protein cultivars. The method was found to be slightly more effective in the identification of high yielding lines with high protein percentage. Furthermore, the single cross method is preferable over the backcross, due to its simplicity of implementation.

APPENDIX A. MEAN VALUES FOR THE SEVEN TRAITS OF BC_1F_3-DERIVED AND F_4-DERIVED LINES AND VINTON 81 FOR THREE CROSSES AT INDIVIDUAL LOCATION IN 1984

Table A1. Mean values for four traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Hardin cross at Manson in 1984

Generation and parent	Trait			
	Yield	Seed weight	Protein	Oil
	($g\ m^{-2}$)	mg/sd	%	%
BC_1F_3	215	188	42.2	20.2
F_4	217	171	41.4	20.4
Vinton 81	193	204	43.0	19.8
L.S.D.$_{0.05}$ (BC_1F_3 vs F_4)	7	3	0.3	0.3
L.S.D.$_{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	20	8	0.9	0.7

Table A2. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Hardin cross at Ames in 1984

Generation and parent	Trait						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	247	9.9	1.7	91	167	41.3	21.4
F_4	252	9.3	2.1	89	152	40.1	21.8
Vinton 81	260	9.5	1.5	91	187	41.2	21.4
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	ns[a]	0.5	0.1	ns	3	0.2	0.2
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	ns	1.5	0.3	ns	7	0.7	0.5

[a]ns = The mean squares for differences among generations were not significant at ($P > 0.05$), therefore, no L.S.D. value was computed.

Table A3. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Hardin cross at Marshalltown in 1984

Generation and parent	Trait						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	246	9.5	2.7	96	184	43.2	20.0
F_4	246	8.8	2.9	95	160	42.6	20.4
Vinton 81	254	9.8	2.1	100	210	43.5	20.0
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	ns[a]	0.5	0.1	ns	4	0.2	0.2
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	ns	1.5	0.3	ns	11	0.6	0.6

[a]ns = The mean squares for differences among generations were not significant at ($P > 0.05$), therefore no L.S.D. value was computed.

Table A4. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Pride B216 cross at Ames in 1984

Generation and parent	Trait						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	264	9.8	1.8	92	170	41.0	21.8
F_4	271	10.3	2.0	90	155	40.2	22.0
Vinton 81	269	8.8	1.7	95	189	42.3	21.2
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	ns[a]	0.5	0.1	2	3	0.2	0.2
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	ns	1.5	0.3	5	9	0.7	0.5

[a] ns = The mean squares for differences among generations were not significant at ($P > 0.05$), therefore, no L.S.D. value was computed.

Table A5. Mean values for seven straits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Pride B216 cross at Marshalltown in 1984

Generation and parent	Trait						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	271	12.7	2.7	94	200	42.9	20.1
F_4	277	13.6	2.7	93	187	42.1	20.3
Vinton 81	267	9.0	2.2	96	212	43.4	19.7
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	ns[a]	0.6	0.1	ns	2	0.2	0.2
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	ns	1.8	0.3	ns	7	0.6	0.5

[a]ns = The mean squares for differences among generations were not significant at ($P > 0.05$), therefore, no L.S.D. value was computed.

Table A6. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Pride B216 cross at Stuart in 1984

Generation	Trait						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	233	9.1	2.0	95	178	41.0	21.3
F_4	236	10.0	2.0	92	164	40.5	21.5
Vinton 81	221	7.3	1.6	93	188	41.4	21.2
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	4	0.4	0.1	1	2	0.3	ns[a]
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	13	1.0	0.3	4	6	0.9	ns

[a]ns = The mean squares for differences among generations were not significant at ($P > 0.05$), therefore no L.S.D. value was computed.

Table A7. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Cumberland cross at Ames in 1984

Generation and parent	Trait						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	237	13.9	2.2	99	169	40.8	21.2
F_4	255	16.4	2.5	100	161	39.7	21.6
Vinton 81	241	8.2	1.7	94	181	42.1	20.8
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	10	0.6	0.1	2	3	0.3	0.2
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	28	1.8	0.3	5	8	0.7	0.5

Table A8. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Cumberland cross at Stuart in 1984

Generation and parent	Trait						
	Yield	Maturity	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	days	score	cm	mg/sd	%	%
BC_1F_3	225	13.4	2.2	98	184	41.0	21.1
F_4	236	16.6	2.2	96	174	39.8	21.7
Vinton 81	212	7.0	1.7	98	190	41.8	21.0
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	4	0.6	0.1	ns[a]	2	0.2	0.1
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	12	1.8	0.3	ns	5	0.6	0.3

[a] ns = The mean squares for differences among generations were not significant at ($P > 0.05$), therefore, no L.S.D. value was computed.

Table A9. Mean values for seven traits of BC_1F_3-derived and F_4-derived lines and Vinton 81 from the Vinton 81 x Cumberland cross at Ottumwa in 1984

Generation and parent	Trait					
	Yield	Lodging	Height	Seed weight	Protein	Oil
	($g\ m^{-2}$)	score	cm	mg/sd	%	%
BC_1F_3	293	3.8	103	187	41.7	20.5
F_4	307	3.7	102	174	40.6	20.9
Vinton 81	257	3.3	95	195	42.1	20.5
$L.S.D._{0.05}$ (BC_1F_3 vs F_4)	8	0.2	3	2	0.3	0.2
$L.S.D._{0.05}$ (Vinton 81 vs BC_1F_3 or F_4)	24	0.5	8	6	0.7	0.5

APPENDIX B. MEAN VALUES FOR SEVEN TRAITS OF BC_1F_3-DERIVED AND F_4-DERIVED LINES, PARENTS, AND CHECK CULTIVARS FOR THE THREE CROSSES AVERAGED ACROSS THREE LOCATIONS IN 1984

Table B1. Mean values for the BC_1F_3-derived and F_4-derived lines, parents and check cultivars for the Vinton 81 x Hardin cross averaged across locations in 1984

Entry Designation	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			BC_1F_3-derived lines				
A84-473001	241	10.5	1.8	94	186	42.2	20.8
02	253	11.0	2.2	102	190	43.5	20.4
03	234	9.2	2.6	91	198	43.2	20.0
04	232	10.2	1.8	92	186	42.0	20.5
05	228	12.2	3.3	104	170	42.1	20.8
06	244	9.0	2.3	98	198	42.3	21.1
07	232	8.2	2.3	90	176	42.4	20.6
08	240	5.2	2.5	84	154	41.4	21.3
09	240	8.5	2.1	97	188	42.6	20.5
10	227	8.0	2.4	94	173	42.1	20.6
11	255	16.8	2.6	105	141	41.8	20.2
12	234	6.5	2.2	91	182	42.6	20.3
13	233	9.0	2.4	96	177	43.0	20.3
14	243	11.0	2.0	96	191	42.3	20.5
15	227	8.8	2.5	90	170	41.8	20.5
16	226	6.2	1.7	89	178	41.3	20.8
17	223	8.8	1.9	98	180	41.5	20.5
18	243	14.0	2.0	101	181	42.8	19.9
19	243	9.8	1.7	93	189	41.0	21.0
20	203	8.2	1.4	85	196	42.5	20.3
21	224	6.0	1.5	82	203	41.0	21.6
22	243	8.8	1.7	90	189	40.5	21.8
23	227	9.0	2.3	93	174	41.9	21.1
24	212	9.0	2.6	87	172	42.7	19.9
25	228	14.2	2.9	106	142	42.6	19.8
26	250	9.8	2.0	98	190	42.6	20.6
27	248	11.2	3.0	101	164	42.2	20.4
28	233	8.8	1.7	81	206	43.0	20.3
29	257	14.8	2.5	90	183	42.9	19.9
30	235	8.2	1.9	82	186	42.9	20.5
31	233	6.5	2.6	92	106	42.5	20.0
32	255	13.2	2.5	100	171	42.1	20.0

Table B1. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			F_4-derived lines				
33	234	8.8	2.4	91	203	41.5	20.4
34	214	4.8	1.4	86	173	41.2	21.7
35	240	9.0	1.8	87	167	41.4	20.8
36	237	7.8	2.8	92	147	40.6	21.6
37	243	4.5	2.9	86	145	40.2	21.9
38	233	5.0	2.1	90	167	42.5	20.2
39	215	7.2	1.7	89	184	43.6	20.3
40	253	6.0	2.1	94	173	41.9	21.3
41	224	3.5	3.8	94	157	40.4	21.6
42	234	5.8	2.5	85	150	40.3	21.6
43	233	6.2	1.8	87	149	40.8	21.0
44	245	11.5	2.6	94	152	41.3	20.7
45	228	6.5	2.5	91	151	40.8	21.3
46	230	15.2	2.7	101	173	43.1	20.0
47	250	11.2	2.8	93	153	42.0	21.1
48	249	10.2	2.9	94	159	41.1	20.6
49	250	12.2	4.0	98	152	41.8	20.7
50	229	9.8	1.7	87	152	40.5	21.4
51	243	9.2	2.4	90	168	41.1	21.4
52	259	14.5	2.4	102	154	41.1	21.1
53	239	10.2	2.1	87	172	42.6	20.4
54	241	9.5	2.9	92	174	41.4	21.1
55	242	13.0	3.2	102	153	41.7	19.5
56	240	12.2	2.0	101	174	41.9	20.0
57	256	12.8	3.3	98	167	39.3	20.5
58	244	9.8	3.1	97	151	42.0	21.4
59	252	8.2	2.8	85	163	41.3	21.3
60	223	8.5	1.5	78	171	41.0	21.2
61	238	8.5	2.3	104	158	41.5	20.5
62	246	12.8	2.9	98	144	42.2	20.6
63	247	9.8	1.9	85	156	39.9	21.1
64	207	5.2	2.2	93	148	41.7	20.2

Table B1. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			Recurrent Parent				
Vinton 81	236	9.6	1.8	95	200	42.4	20.4
			Non-Recurrent Parent				
Hardin	244	6.4	2.1	89	132	40.0	22.0
			Check Cultivars				
Pride B216	267	11.0	2.5	88	136	40.0	21.7
Corsoy 79	253	8.0	1.9	92	137	39.8	22.0
L.S.D.(0.05)	21	1.7	0.2	8	9	0.7	0.5

Table B2. Mean values for the BC_1F_3-derived and F_4-derived lines, parents and check cultivars for the Vinton 81 x Pride B216 cross averaged across locations in 1984

Entry Designation	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			BC_1F_3-derived lines				
A84-474001	268	8.2	1.8	92	182	42.1	21.2
02	253	11.2	2.1	101	188	41.3	21.3
03	251	12.5	2.1	96	179	41.4	21.0
04	262	6.6	2.1	88	168	41.6	21.3
05	279	9.7	2.0	96	172	41.3	21.1
06	269	12.7	1.9	99	177	41.6	21.3
07	236	12.2	2.5	94	184	41.1	21.1
08	264	11.8	2.1	92	196	40.8	21.2
09	234	7.5	1.7	90	170	42.1	21.1
10	255	15.5	2.1	94	184	42.5	20.6
11	258	9.8	2.0	93	181	41.8	21.1
12	261	13.0	2.7	104	173	40.9	21.1
13	260	8.2	1.6	84	183	41.2	21.0
14	278	11.5	2.0	102	191	41.3	20.9
15	258	6.7	1.7	94	180	41.4	21.2
16	243	7.3	2.9	96	177	41.6	20.9
17	261	11.8	2.2	93	192	42.4	21.0
18	227	5.3	2.5	85	172	42.8	20.8
19	261	10.7	2.2	94	177	41.4	21.0
20	253	9.2	1.8	95	182	41.0	21.4
21	259	10.2	1.8	94	169	41.5	21.2
22	287	15.2	2.6	99	181	41.2	21.4
23	241	10.5	1.8	84	182	41.9	20.8
24	260	15.5	3.1	104	189	41.6	21.1
25	254	10.8	2.2	100	196	41.8	21.0
26	240	12.0	2.1	82	179	42.6	20.8
27	272	13.0	2.1	101	182	40.9	21.6
28	263	9.8	2.3	99	203	42.2	20.9
29	244	8.8	2.2	85	182	41.4	20.7
30	236	7.7	2.2	87	172	42.4	20.6
31	256	11.5	2.8	102	185	41.9	21.0
32	251	9.7	1.8	82	201	41.3	21.3

Table B2. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			F_4-derived lines				
33	261	11.5	1.9	91	162	39.9	21.5
34	262	9.3	1.9	88	170	41.6	20.9
35	262	10.2	1.8	88	160	41.0	21.5
36	254	8.3	3.1	99	146	39.0	21.9
37	226	5.0	1.8	83	159	41.9	21.1
38	251	15.2	2.1	89	156	41.3	20.8
39	244	6.0	2.0	89	173	40.8	21.2
40	277	13.5	2.9	89	158	40.0	21.4
41	270	12.5	2.1	90	171	41.1	21.9
42	255	8.8	3.2	97	146	40.5	21.4
43	237	7.7	2.2	91	159	41.1	21.1
44	285	11.3	1.7	88	218	42.7	20.8
45	277	11.0	2.5	90	164	41.0	21.2
46	289	15.8	2.4	108	175	41.0	21.3
47	270	13.7	1.9	92	190	41.2	20.7
48	275	15.3	2.5	92	147	40.8	21.3
49	281	13.5	2.8	105	175	41.6	20.7
50	255	9.3	2.9	90	142	40.8	21.1
51	267	13.8	2.3	102	182	41.0	21.2
52	271	10.5	2.0	99	169	40.7	21.0
53	262	10.5	1.9	95	181	40.6	21.5
54	246	7.0	2.0	78	148	40.6	21.8
55	256	12.7	1.8	74	176	41.1	21.3
56	247	12.0	2.2	81	175	40.8	21.5
57	241	14.7	2.0	86	174	41.2	21.2
58	253	10.7	1.8	92	189	41.6	21.1
59	283	13.3	2.3	101	157	39.8	22.1
60	243	10.0	2.3	92	166	41.4	20.8
61	274	11.7	2.3	86	174	41.4	20.9
62	266	14.2	1.9	97	174	40.3	21.1
63	266	8.3	2.3	91	167	41.1	21.7
64	254	14.2	2.1	96	181	40.8	21.2

Table B2. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			Recurrent Parent				
Vinton 81	252	8.4	1.8	94	196	42.3	20.8
			Non-Recurrent Parent				
Pride B216	272	11.2	2.6	86	143	40.0	21.8
			Check Cultivars				
Pella	299	18.7	2.0	94	178	39.8	21.8
Corsoy 79	268	8.3	2.1	98	136	40.4	21.7
L.S.D.$_{(0.05)}$	20	1.4	0.3	5	7	0.7	0.4

Table B3. Mean values for the BC_1F_3-derived and F_4-derived lines, parents and check cultivars for the Vinton 81 x Cumberland cross averaged across locations in 1984

Entry Designation	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			BC_1F_3-derived lines				
A84-475001	244	15.5	3.0	94	182	41.4	21.1
02	275	19.5	3.4	110	146	39.5	21.2
03	223	9.0	2.4	96	218	43.1	21.0
04	230	9.0	2.4	92	191	41.7	20.9
05	273	16.8	2.9	99	174	40.1	20.5
06	259	16.0	3.1	103	177	39.6	21.2
07	220	21.0	3.2	112	179	41.7	20.4
08	234	8.5	3.0	98	206	42.7	20.7
09	226	8.8	2.8	94	177	42.6	20.4
10	267	19.8	2.4	108	169	40.3	21.0
11	205	24.5	3.6	102	181	40.3	20.3
12	247	10.0	2.6	99	173	40.9	21.3
13	292	14.0	3.2	102	156	9.9	21.4
14	270	16.2	2.4	114	182	40.9	20.6
15	272	20.8	2.5	98	186	39.9	21.1
16	233	13.8	3.3	104	171	42.3	20.1
17	228	8.8	2.0	81	196	41.7	21.2
18	251	14.8	2.9	103	172	41.7	20.5
19	265	17.2	2.3	106	189	40.6	20.9
20	245	13.8	2.7	103	192	40.4	21.4
21	261	8.8	2.0	90	189	41.2	21.7
22	250	15.2	2.6	102	154	41.4	20.1
23	248	11.5	3.3	104	177	41.3	21.5
24	248	10.2	2.3	95	191	41.8	20.8
25	242	7.0	2.2	98	194	42.0	20.7
26	255	11.0	2.1	98	180	40.6	21.2
27	235	8.5	3.1	97	190	43.2	20.4
28	227	15.2	3.1	89	187	41.9	20.0
29	286	19.0	2.6	108	163	40.6	20.3
30	276	9.0	2.6	102	166	41.0	21.0
31	304	9.8	2.2	96	168	40.5	21.8
32	256	13.2	3.1	101	177	40.6	21.8

Table B3. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			F_4-derived lines				
33	275	17.0	2.4	90	181	40.0	22.2
34	259	17.8	3.0	87	170	39.8	21.4
35	271	19.2	2.4	95	155	40.0	21.4
36	267	16.2	3.4	102	178	39.3	20.2
37	266	14.2	2.8	94	158	39.2	21.5
38	302	22.2	2.7	108	156	40.9	21.0
39	262	13.8	3.6	100	164	40.0	21.4
40	255	15.2	3.6	100	163	40.5	21.2
41	251	12.2	3.0	112	180	40.4	21.4
42	247	19.0	2.8	105	153	39.3	21.4
43	279	16.5	2.4	100	175	40.2	21.6
44	260	19.2	2.3	98	175	39.9	20.6
45	259	13.2	3.6	98	160	39.2	22.1
46	237	9.5	3.7	102	162	39.0	22.1
47	262	20.5	3.2	99	152	40.0	22.1
48	278	23.5	3.3	96	177	40.0	21.1
49	271	10.5	1.7	95	213	42.7	21.1
50	294	18.8	2.6	110	176	39.6	22.2
51	256	20.5	2.4	106	172	40.7	20.9
52	255	14.8	3.0	101	180	40.7	21.8
53	292	19.2	3.4	94	155	37.6	21.9
54	303	19.0	3.3	102	165	40.0	21.8
55	257	15.0	2.0	99	173	40.5	21.2
56	264	14.5	2.2	89	166	39.1	20.7
57	264	18.0	3.3	99	164	40.7	21.5
58	218	7.5	2.3	87	166	41.5	21.0
59	265	19.0	2.6	102	161	39.5	21.6
60	270	14.5	3.1	104	168	39.8	21.9
61	245	15.8	2.0	108	185	41.1	21.0
62	276	17.8	2.3	91	185	40.2	20.6
63	274	15.0	2.1	100	167	40.3	21.0
64	275	18.5	2.9	107	161	39.4	21.8

Table B3. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
Recurrent Parent							
Vinton 81	237	7.6	2.2	95	188	42.0	20.8
Non-Recurrent Parent							
Cumberland	285	20.5	2.2	94	152	38.6	22.4
Check Cultivars							
Pella	312	18.0	2.2	96	172	38.1	22.7
Pride B216	282	9.2	2.8	90	134	40.2	21.5
L.S.D. (0.05)	21	2.1	0.4	6	6	0.6	0.4

APPENDIX C. MEAN VALUES FOR SEVEN TRAITS OF LINES FROM THREE CROSSES AT INDIVIDUAL LOCATIONS AND COMBINED ACROSS LOCATIONS IN 1984

Table C1. Mean values for seven traits at individual locations and combined across locations for the three crosses in 1984

Location	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			Vinton 81 x Hardin				
Manson	215	-[a]	-	-	180	41.8	20.3
Ames	250	9.6	1.9	90	160	40.7	21.6
Marshalltown	246	9.2	2.8	96	175	42.9	20.2
Mean	237	9.4	2.4	93	171	41.8	20.7
			Vinton 81 x Pride B216				
Ames	267	10.0	1.9	91	163	40.7	21.9
Marshalltown	274	13.0	2.6	94	194	42.5	20.2
Stuart	234	9.4	2.0	94	171	40.8	21.4
Mean	258	10.8	2.2	93	176	41.3	21.1
			Vinton 81 x Cumberland				
Ames	246	14.9	2.3	99	165	40.3	21.4
Stuart	230	14.7	2.2	97	179	40.4	21.4
Ottumwa	298	-	3.7	102	180	41.2	20.7
Mean	258	14.8	2.7	100	175	40.6	21.1

[a]Indicates that no data were collected.

APPENDIX D. MEAN VALUES FOR SEVEN TRAITS OF BC_1F_3-DERIVED AND F_4-DERIVED LINES, PARENTS AND CHECK CULTIVARS FOR THREE CROSSES AVERAGED ACROSS LOCATIONS IN 1983 AND 1984

Table D1. Mean values for the BC_1F_3-derived and F_4-derived lines, parents and check cultivars for the Vinton 81 x Hardin cross averaged across locations in 1983 and 1984

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			BC_1F_3-derived lines				
A83-204004	209	19.5	2.2	101	186	42.8	20.9
A84-473001	241	10.5	1.8	94	186	42.2	20.8
A83-204005	194	20.5	3.0	106	196	43.9	21.0
A84-473002	253	11.0	2.2	102	190	43.5	20.4
A83-204007	199	20.9	2.2	94	204	42.6	20.6
A84-473003	234	9.2	2.6	91	198	43.2	20.6
A83-204009	218	20.8	2.1	110	192	43.3	20.6
A84-473004	232	10.0	1.8	92	186	42.0	20.5
A83-204014	230	26.0	2.3	103	194	42.2	21.2
A84-473005	228	12.2	3.3	104	170	42.1	20.8
A83-204015	174	20.2	2.4	100	195	42.7	21.4
A84-473006	244	9.0	2.3	98	198	42.3	21.1
A83-205001	202	20.0	2.2	94	199	42.4	21.3
A84-473007	232	8.2	2.3	90	176	42.4	20.6
A83-205002	176	17.8	2.5	79	160	40.9	22.3
A84-473008	240	5.2	2.5	84	154	41.4	21.3
A83-205003	189	18.8	2.2	96	202	44.1	20.4
A84-473009	240	8.5	2.1	97	188	42.6	20.5
A83-205005	174	19.8	2.1	95	172	42.8	20.5
A84-473010	227	8.0	2.4	94	173	42.1	20.6
A83-205006	257	30.0	2.3	116	-	-	-
A84-473011	255	16.8	2.6	105	141	41.8	20.2
A83-205009	220	19.2	2.3	94	195	41.9	21.5
A84-473012	234	6.5	2.2	91	182	42.6	20.3
A83-205015	187	20.0	2.4	86	186	42.6	21.0
A84-473013	233	9.0	2.4	96	177	43.0	20.3
A83-205016	196	20.5	2.4	98	204	42.7	20.3
A84-473014	243	11.0	2.0	96	191	42.3	20.5
A83-206020	221	21.8	2.2	98	184	42.2	21.2
A84-473015	227	8.8	2.5	90	170	41.8	20.5
A83-206023	152	15.5	1.9	92	180	41.8	21.6
A84-473016	226	6.2	1.7	89	178	41.3	20.8
A83-206025	165	19.2	2.4	93	180	40.2	21.9
A84-473017	223	8.8	1.9	98	180	41.5	20.5
A83-206030	218	30.0	2.2	104	-	-	-

Table D1. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A84-473018	243	14.0	2.0	101	181	42.8	19.9
A83-206031	170	19.8	1.8	86	188	40.6	21.4
A84-473019	243	9.8	1.7	93	189	41.0	21.0
A83-206032	182	13.5	1.7	84	-	-	-
A84-473020	203	8.2	1.4	85	196	42.5	20.3
A83-206033	154	16.5	1.8	76	212	40.6	22.2
A84-473021	224	6.9	1.5	82	203	41.0	21.6
A83-206034	190	22.8	1.8	84	198	40.6	22.4
A84-473022	243	8.8	1.7	90	189	40.5	21.8
A83-207019	192	20.2	2.0	92	191	44.1	21.1
A84-473023	227	9.0	2.3	93	174	41.9	21.1
A83-207020	186	24.8	2.9	87	184	43.1	20.4
A84-473024	212	9.0	2.6	87	172	42.7	20.4
A83-207021	198	28.5	2.5	103	-	-	-
A84-473025	228	14.2	2.9	106	142	42.6	19.8
A83-207024	209	17.8	2.2	96	191	42.9	20.9
A84-473026	250	9.8	2.0	98	190	42.6	20.6
A83-207025	217	26.8	2.6	101	-	-	-
A84-473027	248	11.2	3.0	101	164	42.2	20.4
A83-207027	199	18.8	1.9	83	202	43.0	20.9
A84-473028	233	8.8	1.7	81	206	43.0	20.3
A83-207028	196	27.0	2.3	92	-	-	-
A84-473029	257	14.8	2.5	90	183	42.9	19.9
A83-207030	191	22.0	2.1	79	201	42.7	21.7
A84-473030	235	8.2	1.9	82	186	42.9	20.5
A83-207031	170	18.5	2.7	94	169	42.2	20.5
A84-473031	233	6.5	2.6	92	160	42.5	20.0
A83-207034	244	27.8	2.2	107	-	-	-
A84-473032	255	13.2	2.5	100	171	42.1	20.0
			F_4-derived lines				
A83-204018	208	22.8	2.4	98	209	42.6	20.2
A84-473033	234	8.8	2.4	91	203	41.5	20.4
A83-204020	139	13.0	2.1	86	-	-	-
A84-473034	214	4.8	1.4	86	173	41.2	21.7
A83-204021	233	26.8	2.3	91	-	-	-

Table DI. (continued)

Entry Designation	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A84-473035	240	9.0	1.8	87	167	41.4	20.8
A83-204025	189	24.0	2.3	97	151	41.1	21.0
A84-473036	237	7.8	2.8	92	147	40.6	21.6
A83-204026	220	23.5	2.7	105	161	38.8	22.9
A84-473037	243	4.5	2.9	86	145	40.2	21.9
A83-204029	170	14.0	2.5	91	-	-	-
A84-473038	233	5.0	2.1	90	167	42.5	20.2
A83-204034	169	18.8	2.3	94	176	43.2	21.2
A84-473039	215	7.2	1.7	89	184	43.6	20.3
A83-205018	189	22.2	2.4	93	184	43.4	21.5
A84-473040	253	6.0	2.1	94	173	41.9	21.3
A83-205019	183	23.5	3.3	99	171	40.1	22.1
A84-473041	224	3.5	3.8	94	157	40.4	21.6
A83-205021	187	24.0	2.4	86	158	40.2	21.9
A84-473042	234	5.8	2.5	85	150	40.3	21.6
A83-205023	167	15.0	2.4	83	-	-	-
A84-473043	233	6.2	1.8	87	149	40.8	21.0
A83-205026	220	28.0	2.4	98	-	-	-
A84-473044	245	11.5	2.6	94	152	41.3	20.7
A83-205028	202	24.8	2.2	97	165	41.1	22.0
A84-473045	228	6.5	2.5	91	151	40.8	21.3
A83-205029	205	27.2	2.3	98	-	-	-
A84-473046	230	15.2	2.7	101	173	43.1	20.0
A83-205030	211	27.5	2.5	84	-	-	-
A84-473047	250	11.2	2.8	93	153	42.0	21.1
A83-205031	222	26.2	2.5	107	162	42.3	20.4
A84-473048	249	10.2	2.9	94	159	41.1	20.6
A83-206003	222	28.0	2.8	113	-	-	-
A84-473049	250	12.2	4.0	98	152	41.8	20.7
A83-206004	195	27.0	2.1	83	-	-	-
A84-473050	229	9.8	1.7	87	152	40.5	21.3
A83-206006	189	24.0	2.4	98	184	40.6	22.6
A84-473051	243	9.2	2.4	90	168	41.1	21.4
A83-206007	210	26.5	1.9	108	-	-	-
A84-473052	259	14.5	2.4	102	154	41.1	21.1
A83-206008	207	22.8	2.3	86	180	42.9	21.0
A84-473053	239	10.2	2.1	87	172	42.6	20.4

Table D1. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A83-206009	232	26.2	2.4	100	176	41.1	21.8
A84-473054	241	9.5	2.9	92	174	41.4	21.1
A83-206012	245	28.0	2.4	102	-	-	-
A84-473055	242	13.0	3.2	102	153	41.7	19.5
A83-206015	214	25.8	2.2	99	-	-	-
A84-473056	240	12.2	2.0	101	174	41.9	20.0
A83-206016	253	27.5	2.3	97	-	-	-
A84-473057	256	12.8	3.3	98	167	39.3	20.5
A83-207002	214	23.8	2.6	118	154	42.0	22.1
A84-473058	244	9.8	3.1	97	151	42.0	21.4
A83-207004	158	18.8	1.9	78	156	41.1	21.5
A84-473059	252	8.2	2.8	85	163	41.3	21.3
A83-207005	170	24.2	2.0	77	184	42.2	21.3
A84-473060	223	8.5	1.5	78	171	41.0	21.2
A83-207009	189	25.5	2.7	98	-	-	-
A84-473061	238	8.5	2.3	104	158	41.5	20.5
A83-207010	232	26.5	3.6	104	141	43.8	20.4
A84-473062	246	12.8	2.9	98	144	42.2	20.6
A83-207012	210	22.8	2.1	90	155	40.9	21.2
A84-473063	247	9.8	1.9	85	156	39.9	21.1
A83-207015	177	22.0	2.9	87	161	42.6	20.2
A84-473064	207	5.2	2.2	93	148	41.7	20.2
Recurrent Parent							
Vinton 81[a]	186	22.5	2.4	96	197	42.6	20.8
Vinton 81[b]	236	9.6	1.8	95	200	42.4	20.4
Non-Recurrent Parent							
Hardin[a]	169	19.2	2.2	88	135	40.0	22.4
Hardin[b]	244	6.4	2.1	89	132	40.0	22.0

[a]Indicates data from 1983 trial.

[b]Indicates data from 1984 trial.

Table D1. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			Check Cultivars				
Corsoy 79[b]	253	8.0	1.9	92	137	39.8	22.0
Pride B216[b]	267	11.0	2.5	88	136	40.0	21.7
L.S.D.$_{(0.05)}$[a]	33	3.2	0.4	9	9	1.0	0.6
L.S.D.$_{(0.05)}$[b]	21	1.7	0.2	8	9	0.7	0.5

Table D2. Mean values for the BC_1F_3-derived and F_4-derived lines, parents and check cultivars for the Vinton 81 x Pride B216 cross averaged across locations in 1983 and 1984

Entry Designation	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			BC_1F_3-derived lines				
A83-204052	218	16.8	2.4	93	-	-	-
A84-474001	268	8.2	1.8	92	182	42.1	21.2
A83-204054	208	22.2	1.9	109	202	43.1	21.1
A84-474002	253	11.2	2.1	101	188	41.3	21.3
A83-204058	191	26.8	2.2	103	-	-	-
A84-474003	251	12.5	2.1	96	179	41.4	21.0
A83-204059	219	17.0	2.1	98	-	-	-
A84-474004	262	6.6	2.1	88	186	41.6	21.3
A83-204061	230	24.8	2.5	98	175	42.1	20.8
A84-474005	279	9.7	2.0	96	172	41.3	21.1
A83-204063	203	25.8	2.2	104	-	-	-
A84-474006	269	12.7	1.9	99	177	41.6	21.3
A83-204064	204	24.0	2.3	101	195	42.7	20.8
A84-474007	236	12.2	2.5	94	184	41.1	21.1
A83-204065	222	21.2	2.4	99	210	41.1	21.6
A84-474008	264	11.8	2.1	92	196	40.8	21.2
A83-204067	170	16.5	1.9	82	-	-	-
A84-474009	234	7.5	1.7	90	170	42.1	21.1
A83-205053	213	26.8	2.1	95	-	-	-
A84-474010	255	15.5	2.1	94	184	42.5	20.6
A83-205054	189	22.0	2.3	94	186	41.8	21.0
A84-474011	258	9.8	2.0	93	181	41.8	21.1
A83-205056	202	24.2	2.2	98	180	41.0	21.2
A84-474012	261	13.0	2.7	104	173	40.9	21.1
A83-205060	212	19.2	2.4	82	-	-	-
A84-474013	260	8.2	1.6	84	183	41.2	21.0
A83-205062	215	23.8	2.4	98	200	41.9	21.2
A84-474014	278	11.5	2.0	102	191	41.3	20.9
A83-205063	220	17.2	2.2	105	-	-	-
A84-474015	258	6.7	1.7	94	180	41.4	21.2
A83-205066	210	21.0	2.3	102	184	42.4	21.0
A84-474016	243	7.3	2.9	96	177	41.6	20.9
A83-206052	213	22.8	2.0	93	202	43.3	21.2
A84-474017	261	11.8	2.2	93	192	42.4	21.0
A83-206054	218	20.5	2.4	92	191	42.2	21.7

Table D2. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A84-474018	227	5.3	2.5	85	172	42.8	20.8
A83-206057	237	19.2	2.1	101	-	-	-
A84-474019	261	10.7	2.2	94	177	41.4	21.0
A83-206059	213	23.0	1.8	93	198	41.3	21.8
A84-474020	253	9.2	1.8	95	182	41.0	21.4
A83-206061	239	22.2	1.8	96	181	42.2	21.3
A84-474021	259	10.2	1.8	94	169	41.5	21.2
A83-206063	190	27.2	2.4	101	-	-	-
A84-474022	287	15.2	2.6	99	181	41.2	21.4
A83-206065	214	22.0	2.0	90	194	42.5	21.1
A84-474023	241	10.5	1.8	84	182	41.9	20.8
A83-206068	231	25.8	2.2	100	-	-	-
A84-474024	260	15.5	3.1	104	189	41.6	21.1
A83-207053	192	23.5	1.8	95	209	43.4	21.1
A84-474025	254	10.8	2.2	100	196	41.8	21.0
A83-207055	204	23.8	1.8	81	176	43.8	20.5
A84-474026	240	12.0	2.1	82	179	42.6	20.8
A83-207056	202	24.2	2.1	93	186	42.1	21.5
A84-474027	272	13.0	2.1	101	182	40.9	21.6
A83-207059	210	21.0	2.1	94	-	-	-
A84-474028	263	9.8	2.3	99	203	42.2	20.9
A83-207061	186	19.8	2.3	86	-	-	-
A84-474029	244	8.8	2.2	85	182	41.4	20.7
A83-207063	228	19.8	2.2	89	-	-	-
A84-474030	236	7.7	2.2	87	172	42.4	20.6
A83-207066	216	25.2	2.3	96	202	43.5	21.0
A84-474031	256	11.5	2.8	102	185	41.9	21.0
A83-207067	204	23.5	1.9	89	204	43.1	20.8
A84-474032	251	9.7	1.8	82	201	41.3	21.3
			F_4-derived lines				
A83-204036	209	20.0	2.0	95	-	-	-
A84-474033	261	11.5	1.9	91	162	39.9	21.5
A83-204037	208	20.2	2.2	87	-	-	-
A84-474034	262	9.3	1.9	88	170	41.6	20.9
A83-204039	217	21.8	2.2	94	179	41.0	22.2

Table D2. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A84-474035	262	10.2	1.8	88	160	41.0	21.5
A83-204043	216	20.0	2.2	97	-	-	-
A84-474036	254	8.3	3.1	99	146	39.0	21.9
A83-204045	182	18.2	2.4	90	-	-	-
A84-474037	226	5.0	1.8	83	159	41.9	21.1
A83-204047	236	26.5	1.9	101	-	-	-
A84-474038	251	15.2	2.1	89	156	41.3	20.8
A83-204049	205	14.2	2.0	89	-	-	-
A84-474039	244	6.0	2.0	89	173	40.8	21.2
A83-204051	236	24.0	2.3	97	174	41.0	21.8
A84-474040	277	13.5	2.9	89	158	40.0	21.4
A83-205036	256	26.0	2.0	98	189	41.8	22.2
A84-474041	270	12.5	2.1	90	171	41.1	21.9
A83-205037	219	21.2	2.4	109	165	40.3	22.0
A84-474042	255	8.8	3.2	97	146	40.5	21.4
A83-205038	201	23.2	1.9	91	189	40.7	21.8
A84-474043	237	7.7	2.2	91	159	41.1	21.1
A83-205040	222	22.2	2.0	90	229	43.4	21.1
A84-474044	285	11.3	1.7	88	218	42.7	20.8
A83-205042	247	23.2	2.1	95	184	41.4	22.0
A84-474045	277	11.0	2.5	90	164	41.0	21.2
A83-205043	227	27.2	2.2	108	-	-	-
A84-474046	289	15.8	2.4	108	175	41.0	21.3
A83-205045	221	26.0	1.9	99	-	-	-
A84-474047	270	13.7	1.9	92	190	41.2	20.7
A83-205046	295	27.2	2.1	102	-	-	-
A84-474048	275	15.3	2.5	92	147	40.8	21.3
A83-205047	193	22.8	2.2	107	191	42.4	20.9
A84-474049	281	13.5	2.8	105	175	41.6	20.7
A83-205049	231	22.2	2.1	95	161	41.2	22.1
A84-474050	255	9.3	2.9	90	142	40.8	21.1
A83-206035	215	27.8	2.5	112	-	-	-
A84-474051	267	13.8	2.3	102	182	41.0	21.2
A83-206040	217	21.2	2.0	92	175	41.6	21.4
A84-474052	271	10.5	2.0	99	169	40.7	21.0
A83-206043	231	23.5	2.0	98	190	41.7	22.0
A84-474053	262	10.5	1.9	95	181	40.6	21.5

Table D2. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A83-206047	212	21.0	2.1	90	160	40.9	22.2
A84-474054	246	7.0	2.0	78	148	40.6	21.8
A83-206048	231	25.5	1.7	82	-	-	-
A84-474055	256	12.7	1.8	74	176	41.1	21.3
A83-206050	239	26.0	2.2	86	-	-	-
A84-474056	247	12.0	2.2	81	175	40.8	21.5
A83-206051	221	26.5	2.2	92	-	-	-
A84-474057	241	14.7	2.0	86	174	41.2	21.2
A83-207036	192	22.8	2.0	95	209	42.8	21.3
A84-474058	253	10.7	1.8	92	189	41.6	21.1
A83-207038	240	23.2	2.2	111	165	41.0	22.4
A84-474059	283	13.3	2.3	101	157	39.8	22.1
A83-207040	241	22.0	2.5	96	189	41.5	21.2
A84-474060	243	10.0	2.3	92	166	41.4	20.8
A83-207043	221	26.0	1.9	90	-	-	-
A84-474061	274	11.7	2.3	86	174	41.4	20.9
A83-207045	212	24.8	1.9	98	175	41.3	21.2
A84-474062	266	14.2	1.9	97	174	40.3	21.1
A83-207047	222	19.2	2.0	86	-	-	-
A84-474063	266	8.3	2.3	91	167	41.1	21.7
A83-207051	239	25.5	2.4	99	-	-	-
A83-474064	254	14.2	2.1	96	181	40.8	21.2
Recurrent Parent							
Vinton 81[a]	188	22.6	2.4	91	200	42.4	21.2
Vinton 81[b]	252	8.4	1.8	94	196	42.3	20.8
Non-Recurrent Parent							
Pride B216[a]	235	25.6	1.9	89	160	-	-
Pride B216[b]	272	11.2	2.6	86	143	40.0	21.8

[a]Indicates data from 1983 trial.

[b]Indicates data from 1984 trial.

Table D2. (continued)

Entry Designation	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
Check Cultivars							
Corsoy 79[b]	268	8.3	2.1	98	136	40.4	21.7
Pella[b]	299	18.7	2.0	94	178	39.8	21.8
L.S.D.$_{(0.05)}$[a]	30	2.7	0.4	8	11	1.1	0.6
L.S.D.$_{(0.05)}$[b]	20	1.4	0.3	5	7	0.7	0.4

Table D3. Mean values for the BC_1F_3-derived and F_4-derived lines, parents and check cultivars for the Vinton 81 x Cumberland cross averaged across locations in 1983 and 1984

Entry Designation	Yield ($g\ m^{-2}$)	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			BC_1F_3-derived lines				
A83-205090	203	29.0	1.9	103	179	42.8	20.2
A84-475001	244	15.5	3.0	94	182	41.4	21.1
A83-204094	252	31.2	2.8	127	155	41.0	20.4
A84-475002	275	19.5	3.4	110	146	39.5	21.2
A83-204096	206	23.0	2.0	105	250	44.8	20.8
A84-475003	223	9.0	2.4	96	218	43.1	21.0
A83-204097	188	24.8	2.4	93	226	43.4	20.6
A84-475004	230	9.0	2.4	92	191	41.7	20.9
A83-204098	244	31.8	2.6	100	185	41.8	20.0
A84-475005	273	16.8	2.9	99	174	40.1	20.5
A83-204100	193	30.8	2.9	112	171	41.8	20.6
A84-475006	259	16.0	3.1	103	177	39.6	21.2
A83-204101	219	34.5	2.2	122	181	43.5	19.8
A84-475007	220	21.0	3.2	112	179	41.7	20.4
A83-204102	216	22.5	2.4	92	219	44.3	20.4
A84-475008	234	8.5	3.0	98	206	42.7	20.7
A83-205086	193	25.5	2.5	98	199	44.1	20.5
A84-475009	226	8.8	2.8	94	177	42.6	20.4
A83-205090	252	33.2	2.2	120	178	41.0	20.1
A84-475010	267	19.8	2.4	108	169	40.3	21.0
A83-205092	214	36.5	3.0	108	170	42.8	19.3
A84-475011	205	24.5	3.6	102	181	40.3	20.3
A83-205093	192	24.8	1.9	95	181	41.0	21.8
A84-475012	247	10.0	2.6	99	173	40.9	21.3
A83-205095	217	32.0	2.3	100	166	41.5	20.8
A84-475013	292	14.0	3.2	102	156	39.9	21.4
A83-205097	207	33.2	2.3	121	196	43.2	19.7
A84-475014	270	16.2	2.4	114	182	40.9	20.6
A83-205098	218	35.2	2.1	98	176	41.8	20.4
A84-475015	272	20.8	2.5	98	186	39.9	21.0
A83-205099	201	29.5	2.6	112	185	43.9	19.4
A84-475016	233	13.8	3.3	104	171	42.3	20.1
A83-206087	209	23.0	1.7	81	214	41.4	21.7
A84-475017	228	8.8	2.0	81	196	41.7	21.2
A83-206091	235	31.5	2.5	100	181	42.9	20.5

Table D3. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A84-475018	251	14.8	2.9	103	172	41.7	20.5
A83-206093	250	31.0	2.2	114	210	42.3	20.8
A84-475019	265	17.2	2.3	106	189	40.6	20.9
A83-206095	236	29.5	2.4	104	214	41.5	21.4
A84-475020	245	13.8	2.7	103	192	40.4	21.4
A83-206096	184	24.0	2.1	89	194	41.8	21.8
A84-475021	261	8.8	2.0	90	189	41.2	21.7
A83-206097	230	32.0	2.0	96	170	41.9	20.0
A84-475022	250	15.2	2.6	102	154	41.4	20.1
A83-206098	201	20.8	2.2	98	186	41.6	22.0
A84-475023	248	11.5	3.3	104	177	41.3	21.5
A83-206099	221	22.5	2.0	97	212	43.1	21.3
A84-475024	248	10.2	2.3	95	191	41.8	20.8
A83-207087	185	15.5	1.7	94	-	-	-
A84-475025	242	7.0	2.2	98	194	42.0	20.7
A83-207092	205	24.8	2.0	88	182	41.7	21.0
A84-475026	255	11.0	2.1	98	180	40.6	21.2
A83-207094	188	24.5	1.9	88	204	44.7	20.4
A84-475027	235	8.5	3.1	97	190	43.2	20.4
A83-207096	223	32.0	2.4	98	201	43.4	19.4
A84-475028	227	15.2	3.1	89	187	41.9	20.0
A83-207099	237	30.8	2.3	108	164	41.3	20.3
A84-475029	286	19.0	2.6	108	163	40.6	20.3
A83-207100	222	23.2	2.2	97	175	42.9	20.8
Q84-475030	276	9.0	2.6	102	166	41.0	21.0
A83-207101	203	25.5	1.9	96	180	42.7	22.2
A84-475031	304	9.8	2.2	96	168	40.5	22.5
A83-207102	187	24.2	2.2	104	176	42.5	21.2
A84-475032	256	13.2	3.1	101	177	40.6	21.8
			F_4-derived lines				
A83-204069	237	31.0	2.4	103	-	-	-
A84-475033	275	17.0	2.4	90	181	40.0	22.2
A83-204070	268	30.0	2.4	88	192	40.2	21.5
A84-475034	259	17.8	3.0	87	170	39.8	21.4
A83-204076	204	29.5	2.2	98	-	-	-

Table D3. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A84-475035	271	19.2	2.4	95	155	40.0	21.4
A83-204077	238	34.0	2.4	112	178	40.2	19.5
A84-475036	267	16.2	3.4	102	178	39.3	20.2
A83-204078	261	29.0	2.4	101	179	39.6	21.8
A84-475037	266	14.2	2.8	94	158	39.2	21.5
A83-204080	223	30.1	2.3	118	171	43.1	20.2
A84-475038	302	22.2	2.7	108	156	40.9	21.0
A83-204081	204	28.8	3.2	114	184	40.8	21.4
A84-475039	262	13.8	3.6	100	164	40.0	21.4
A83-204083	217	28.5	2.4	97	168	43.0	21.0
A84-475040	255	15.2	3.6	100	163	40.5	21.2
A83-204084	186	27.5	2.8	117	195	40.9	21.0
A84-475041	251	12.2	3.0	112	180	40.4	21.4
A83-205072	194	30.5	2.4	117	-	-	-
A84-475042	247	19.0	2.8	105	153	39.3	21.4
A83-205073	257	30.0	2.4	107	191	41.6	21.5
A84-475043	279	16.5	2.4	100	175	40.2	21.6
A83-205074	215	32.8	2.5	108	181	41.1	20.4
A84-475044	260	19.2	2.3	98	175	39.9	20.6
A83-205075	240	29.0	2.2	105	174	39.8	21.9
A84-475045	259	13.2	3.6	98	160	39.2	22.1
A83-205076	211	22.8	2.0	103	176	38.9	22.8
A84-475046	237	9.5	3.7	102	162	39.0	22.1
A83-205077	239	34.0	2.5	109	152	40.2	21.1
A84-475047	262	20.5	3.2	99	152	40.0	22.1
A83-205078	235	32.8	2.2	104	179	40.8	20.8
A84-475048	278	23.5	3.3	96	177	40.0	21.1
A83-205079	198	23.0	1.7	100	241	44.8	20.4
A84-475049	271	10.5	1.7	95	213	42.7	21.1
A83-205082	267	30.5	2.4	114	182	40.2	21.8
A84-475050	294	18.8	2.6	110	176	39.6	22.2
A83-206069	208	31.0	2.6	104	188	41.5	20.3
A84-475051	256	20.5	2.4	106	172	40.7	20.9
A83-206071	219	29.0	2.2	106	195	42.4	21.2
A84-475052	255	14.8	3.0	101	180	40.7	21.8

Table D3. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
A83-206078	277	29.5	2.2	98	165	37.8	22.0
A84-475053	292	19.2	3.4	94	155	37.6	21.9
A83-206079	245	30.5	2.2	106	175	41.0	21.4
A84-475054	303	19.0	3.3	102	165	40.0	21.8
A83-206080	278	31.5	2.0	111	174	39.8	20.9
A84-475055	257	15.0	2.0	99	173	40.5	21.2
A83-206083	212	34.5	2.3	86	170	39.8	20.4
A84-475056	264	14.5	2.2	89	166	39.1	20.7
A83-206085	256	31.0	2.0	107	170	40.0	21.8
A84-475057	264	18.0	3.3	99	164	40.7	21.5
A83-207071	211	23.8	2.0	90	180	42.9	21.0
A84-475058	218	7.5	2.3	87	166	41.5	21.0
A83-207072	244	32.2	3.0	101	168	40.6	21.4
A84-475059	265	19.0	2.6	102	161	39.5	21.6
A83-207078	266	27.5	2.1	111	175	40.7	21.8
A84-475060	270	14.5	3.1	104	168	39.8	21.9
A83-207079	255	30.0	2.1	106	186	42.2	20.2
A84-475061	245	15.8	2.0	108	185	41.1	21.0
A83-207082	249	30.2	1.9	98	181	41.1	20.5
A84-475062	276	17.8	2.3	91	185	40.2	20.6
A83-207084	252	30.2	2.0	102	171	40.0	21.5
A84-475063	274	15.0	2.1	100	167	40.3	21.0
A83-207085	239	31.0	2.0	114	162	40.6	21.1
A84-475064	275	18.5	2.9	107	161	39.4	21.8
Recurrent Parent							
Vinton 81[a]	178	22.2	2.2	90	200	43.3	20.7
Vinton 81[b]	237	7.6	2.2	95	188	42.0	20.8
Non-Recurrent Parent							
Cumberland[a]	250	32.4	2.0	96	165	39.0	22.0
Cumberland[b]	285	20.5	2.2	94	152	38.6	22.4

[a]Indicates data from 1983 trial.

[b]Indicates data from 1984 trial.

Table D3. (continued)

Entry Designation	Yield (g m^{-2})	Maturity (days)	Lodging (score)	Height (cm)	Seed Weight (mg/sd)	Protein (%)	Oil (%)
			Check Cultivars				
Pella[b]	312	18.0	2.2	96	172	38.1	22.7
Pride B216[b]	282	9.2	2.8	90	134	40.2	21.5
L.S.D.$_{(0.05)}$[a]	34	2.1	0.6	10	11	1.0	0.6
L.S.D.$_{(0.05)}$[b]	21	2.1	0.4	6	6	0.6	0.4

SECTION II. TRANSFER OF PHYTOPHTHORA RESISTANCE IN SOYBEAN [*Glycine max* (L.) Merr.] BY BACKCROSSING

INTRODUCTION

Phytophthora rot, caused by Phytophthora megasperma Drecks. var. sojae Hildeb., is one of the most destructive diseases of soybeans in the United States. On the alluvial soils of the lower Mississippi River Valley, it has been estimated that the disease can cause economic losses to soybean on 2 million hectares (Kilen and Barrentine, 1983). The pathogen causes pre- and post-emergence damping-off of seedlings and a root and stem rot that results in wilting and death of plants from the primary leaf stage to maturity (Kaufmann and Gerdemann, 1958). The disease also may reduce the vigor of susceptible plants and lower yield.

Twenty-four physiologic races of Phytophthora have been reported to cause root and stem rot of soybean. Several genes have been reported that confer resistance against specific races of the pathogen. Thus, breeding for resistance is an important objective for control of this malady.

In the development of soybean cultivars with resistance to phytophthora rot, two strategies for backcrossing usually are employed. One strategy involves yield testing while the other does not involve yield evaluation. For the strategy involving yield testing, selection is made for lines that appear phenotypically similar to the recurrent parent and homozygous for resistance to the disease. Yield tests are conducted to identify the best line for release as a new cultivar. In backcrossing without yield testing, homozygous resistant lines with visual plant characteristics similar to the recurrent parent are selected. Seeds of the selected lines are composited for release as a new cultivar.

Wilcox et al. (1971) evaluated the number of backcrosses required to transfer a gene for phytophthora resistance into five soybean cultivars. They compared the performance of random resistant and susceptible liens selected after each backcross generation. Yields of the resistant and susceptible lines were not significantly less than that of the recurrent parent by the seventh backcross. They concluded that seven backcrosses without selection for agronomic characteristics, followed by elimination of plant rows that did not conform to the phenotype of the recurrent parent, would be the most efficient way to add major genes for phytophthora rot resistance to susceptible cultivars. Their finding indicated that release of a high-yielding cultivar using the backcross procedure would require considerable time. It would be desirable if recovery of high-yielding phenotypes could be made in earlier generations of backcrossing, without the need for expensive and time consuming yield trials. No published information is available to verify the results of Wilcox et al. (1971) and to explore the possibility of recovering superior phenotypes at earlier generations of backcrossing. My study was designed with the following objectives:

1) to determine the number of backcross generations required to transfer a major gene for phytophthora resistance into a cultivar and obtain lines with the yield potential of the recurrent parent, and
2) to determine in what backcross generation a composite of visually similar lines could be made that would yield as much as the recurrent parent.

LITERATURE REVIEW

Inheritance of Resistance to Phytophthora Root and Stem Rot in Soybean

The genetics of resistance to phytophthora rot (caused by Phytophthora megasperma Drecks var. sojae Hildeb.) in soybean has been studied by several authors. Twenty-four physiologic races and genes conferring resistance have been identified and reported (Kilen, 1985) (Table 1).

Bernard et al. (1957) found that resistance to the disease was controlled by a single dominant gene Ps based on inoculation of progenies from crosses between resistant and susceptible cultivars. The designation for the gene was later changed to Rps by Hartwig et al. (1968).

Morgan and Hartwig (1965) identified a second race of the pathogen based on differential reactions of the soybean strain D60-9467 to two isolates. Inheritance studies indicated that resistance to race 2 was controlled by the gene rps^2, which was part of an allelomorphic series. Rps was dominant to rps^2, and rps^2 was dominant to rps (Hartwig et al., 1968). Race 3 was identified by Schmitthenner (1972), race 4 by Schiverk and Sin (1974), races 5 and 6 by Haas and Buzzell (1976), and races 7, 8, 9 by Laviolette (1979), races 10 to 16 by Keeling (1980), races 17 to 20 by Keeling (1982), races 21 and 22 by Laviolette and Athow (1983), race 23 by White et al. (1983), and race 24 by Keeling (1984). The reactions of sixteen differential cultivars to races 1 to 24 of the pathogen are summarized in Table 1.

As new races were identified, genes that provided resistance to specific races of the pathogen have been found. Kilen et al. (1974) reported a dominant gene $\underline{Rps}^2$ in the cultivar CNS based on the reactions of progenies from crosses between CNS-derived lines and susceptible strains to liquid cultures of the pathogen. The authors suggested changing the previously reported locus $\underline{Rps}$, $\underline{rps}^2$, and $\underline{rps}$ to the new designation $\underline{Rps}$, $\underline{rps}_1^2$, and $\underline{rps}_1$ to distinguish it from the second locus. Mueller et al. (1978) identified the gene $\underline{Rps}_1^c$ in PI 54615-1 and suggested changing the $\underline{rps}_1^2$ designation to $\underline{rps}_1^b$, forming the allelic series in decreasing order of dominance from $\underline{Rps}_1^a$, $\underline{Rps}_1^b$, and $\underline{rps}_1$. They also reported that the dominant allele $\underline{Rps}_3$ in PI 86972-1 was at a different locus from those previously reported.

Laviolette et al. (1979) extended the number of physiologic races of the pathogen controlled by specific genes showing that $\underline{Rps}$ controlled resistance to races 1, 3, 4, and 5 through 9 and that $\underline{Rps}_1$ governed resistance to races 1 through 3 and 6 through 9. The independent gene $\underline{Rps}_3$ controlled resistances to races 1 through 4 and 5, 8 and 9. A gene at a new locus, $\underline{Rps}_4$, that governs resistance to races 1 through 4 of the pathogen, was found by Athow et al. (1980). Buzzell and Anderson (1981) reported that the gene $\underline{Rps}_5$ conferred resistance to races 1 through 5, and 8 and 9. Bernard and Cremeens (1981) reported that the allele $\underline{Rps}_1^k$ controlled resistance to races 1 through 10, 13, 14, and 15, but resulted in susceptibility to races 12 and 16. The $\underline{Rps}_6$ gene in the cultivar Altoona was found by Athow and Laviolette (1982). Genes for resistance to specific races of $\underline{Phytophthora}$ are listed in Table 1.

Table 1. Reactions of soybean cultivars with their corresponding genes for resistance to physiologic races of Phytophthora megasperma F. Sp. Glycinea (Adapted from Kilen, 1985)

Source	Gene	Reaction to physiologic race										
		1	2	3	4	5	7	8	9	10	12	13
Harosoy	rps	S	S	S	S	S	S	S	S	S	R	S
Mukden	Rps_1	R	R	S	S	S	S	S	S	R	R	R
Sanga	$Rps_1{}^b$	R	S	R	R	R	R	R	R	S	S	R
Mack	$Rps_1{}^c$	R	R	R	S	S	R	R	R	R	S	R
PI 103091[a]	$Rps_1{}^d$	R	R	R	R	R	R	S	R	R	S	R
Kingwa	$Rps_1{}^k$	R	R	R	R	R	R	R	R	R	S	R
CNS	Rrs_2	R	R	R	R	-	S	S	R	R	R	R
PI 171442	Rps_3	R	R	R	R	R	S	R	R	S	S	R
PI 172901[a]	$Rps_3{}^b$	R	R	R	R	R	R	-	R	R	R	-
PI 340046[a]	$Rps_3{}^c$	R	R	R	R	S	S	-	S	-	R	-
PI 82312N[a]	$Rps_3{}^d$	R	R	R	R	R	S	-	R	-	-	-
PI 273483D[a]	$Rps_3{}^e$	R	R	R	R	S	S	-	S	-	R	-
PI 86050	Rps_4	R	R	R	R	S	S	S	S	R	R	R
T240	Rps_5	R	R	R	R	R	S	R	R	S	S	R
Altona	Rps_6	R	R	R	R	S	S	S	S	R	R	S
PI 82312N[a]	Rps_7	R	R	R	R	R	R	R	R	-	-	-

[a]Gene symbols not published. Symbol R_{ps} - Harosoy suggested for resistant gene in Harosoy. Williams suggested as universally susceptible with rps.

14	15	16	17	18	19	20	21	22	23	24
S	S	R	S	R	R	S	S	S	S	S
S	R	R	R	R	R	S	S	S	S	R
R	R	S	S	R	S	S	R	R	S	S
S	R	S	R	S	S	S	R	S	R	R
R	R	R	S	R	S	R	R	R	R	R
R	R	S	R	R	S	S	R	R	–	–
R	S	S	S	–	–	–	–	–	–	–
R	S	R	S	R	S	S	S	S	R	S
–	–	R	–	–	–	–	–	–	–	–
–	–	R	–	–	–	–	–	–	–	–
–	–	–	–	–	–	–	–	–	–	–
R	–	R	–	–	–	–	–	–	–	–
R	R	R	R	R	R	R	R	S	–	–
R	S	R	S	S	S	–	S	–	–	–
R	R	R	S	R	R	R	R	S	S	S
–	–	–	–	–	–	–	–	–	–	–

Use of the Backcross Method for Transferring a Specific Gene for Resistance to Phytophthora Rot

Backcrossing was proposed by Harlan and Pope (1922) as a method to incorporate a simply inherited character into an existing cultivar that has a large number of desirable characteristics. The method has been used successfully to transfer genes controlling many characters, including disease resistance (Briggs, 1930; Briggs and Allard, 1953; Harlan and Pope, 1922; Suneson, 1945; Thomas, 1952). Briggs and Allard (1953) described three important criteria for a successful backcrossing program, namely 1) the availability of a satisfactory recurrent parent; 2) the retention of a worthwhile intensity of the character being transferred through several backcrosses; and 3) reconstitution of the genotype of the recurrent parent by a reasonable number of backcrosses carried out with a population of manageable size. They indicated that the development of soybean cultivars resistant to P. megasperma Drecks. var. sojae Hildeb. met the above mentioned criteria. Soybean cultivars developed by backcrossing have been designated by the name of the recurrent parent and the year that the backcross derivative was released; Clark 63, Harosoy 63, Hawkeye 63, Lindarin 63, Chippewa 64, Lee 68, Amsoy 71, Cutler 71, and Pickett 71.

The usefulness of the backcrossing procedure for the transfer of major genes for phytophthora rot was evaluated by Wilcox et al. (1971). The study revealed varied results among crosses, but in general, recovery of the recurrent parent phenotype was slower than predicted if only additive genetic control was assumed for the agronomic

characteristics being evaluated. They concluded that seven backcrosses without selection for agronomic characteristics, followed by elimination of progeny rows that did not conform to the phenotype of the recurrent parent would be the most efficient way to add Phytophthora resistance to susceptible cultivars.

Available evidence indicates that seven backcrosses are not always necessary to transfer major genes for phytophthora rot resistance in to susceptible cultivars, based on released cultivars that had fewer backcrosses. Of the 19 cultivars of soybeans released from 1961 until 1985 using the backcross procedure, only 6 cultivars were developed using seven backcrosses. The remaining 13 cultivars involved six or fewer backcrosses (Table 2).

Table 2. Summary of soybean cultivars developed by backcrossing since 1961

Cultivar	Number of Backcross	Pedigree	Reference
Hardin	2	Corsoy x Cutler 71	Fehr et al. (1983)
Cutler 71	3	Cutler x (Kent-Rpsr x p-SL-5	Probst et al. (1971b)
Vickery	4	Corsoy x (L65-1342 x Mack & Anoka x Mack)	Fehr et al. (1981)
Lindarin 63	4	Lindarin x Mukden	Probst et al. (1964)
Vinton 81	4	L60-347-4-4G-2B x Vinton	Fehr et al. (1984)
Union	4	Williams x SL12	Bernard and Cremeens (1982)
Clark 63	a) 4 b) 6	(Clark x S54-1714) x (Clark x Blackhawk)	Williams and Bernard (1964)
Lee 68	5	Lee x Arksoy	Caviness and Walters (1968)
Hawkeye 63	6	Hawkeye x Blackhawk	Bernard (1964)
Keller	6	Beeson 80 x PR x 9-29	Athow et al. (1984a)
Miami	6	Wells II x PR x 9-274	Athow et al. (1984b)
Winchester	6	Williams x PR x 12-112	Athow et al. (1984c)
Hodgson 78	6	Hodgson x Merit	Lambert and Kennedy (1979)
Harosoy 63	7	Harosoy x Blackhawk	Bernard (1964)
Chippewa 64	7	Chippewa x Blackhawk	Bernard (1964)
Amsoy 71	7	Amsoy x C1253	Probst et al. (1972)
Hood 75	7	Hood x Arksoy	Caviness and Walters (1976)
Wells II	7	Wells x Arksoy	Wilcox et al. (1979)
Beeson 80	7	Beeson x Arksoy	Wilcox et al. (1980)

MATERIALS AND METHODS

Crosses were made to transfer resistance to Phytophthora Megasperma Drecks, var. sojae Hildeb. from William 82 into the susceptible genotypes, A78-123018 and Cumberland. The performance of the two recurrent parents and the donor parent is presented in Table 3.

Table 3. Yield and maturity for the recurrent parents and donor parent in 1982

Parent	Yield (bu./acre)	Maturity
Recurrent		
A78-123018[a]	44.8	Sept. 24
Cumberland[b]	49.8	Oct. 5
Donor		
Williams 82[b]	45.2	Oct. 9

[a]Source: U.S. Dept. of Agriculture, 1982.

[b]Source: U.S. Dept. of Agriculture, 1982.

A78-123018 was selected because of its high yield potential and suitable maturity for northern Iowa. Based on a three-year mean from 1980-1982, A78-123018 ranked first among the group I strains tested. Cumberland was selected for its high yield, desirable agronomic characteristics and suitable maturity for southern Iowa. Williams 82 was chosen primarily as the donor of the gene ($\underline{Rps}_1^k$) that confers specific resistance to many specific races of phytophthora rot.

The development of the different generations of A78-123018 Cumberland crosses is outlined in Table 4. Single crosses were made between A78-123018 x Williams 82 and Cumberland x Williams 82 at the Isabela Substation, University of Puerto Rico in January, 1981. Six hybrid seeds of each cross were obtained. In the summer of 1981 at Ames, seven BC_1F_1 seeds were produced by backcrossing the F_1 plants to each of the recurrent parents. Cumberland and A78-123018 were used as male parents for this and all succeeding backcrosses. In the November 1981 planting in Puerto Rico, seven BC_2F_1 seeds were obtained from each Cumberland and A78-123018 BC_1F_1 plants. Twenty BC_1F_2 seeds for every BC_1F_1 plant used for crossing were sent to Ames for progeny testing for phytophthora resistance. BC_3F_1 and BC_2F_2 seeds were produced from BC_2F_1 at Puerto Rico in February 1982. The seven seeds of BC_3F_1 were obtained only on those BC_2F_1 plants test were found resistant based on progeny test.

In the summer of 1982 at Ames, the final backcrosses were made by obtaining 10 BC_4F_1 seeds. During the same season, seeds from previous backcross generation were grown to obtain lines homozygous for Phytophthora resistance. $F_{2:3}$ seeds were obtained from F_2 plants while $BC_1F_{2:3}$ seeds were obtained from BC_1F_2 plants. BC_2F_2 derived line in F_3 seeds were obtained from BC_2F_2 plants in the summer at Puerto Rico, in 1982. In the November 1982 planting in Puerto Rico, $F_{2:4}$ lines were produced from F_3 plants. Also, BC_4F_2 seeds were harvested individually from BC_4F_1 plants. $F_{4:5}$ $BC_1F_{3:4}$ and $BC_3F_{2:3}$ seeds were obtained in February 1983 at Puerto Rico.

Table 4. Outline for the development of different generation of A78-123018 and Cumberland crosses

Planting Date	Location	Operation	
		BC_0	BC_1
Jan 1981	Puerto Rico	F_1 seeds were obtained	F_1 seeds were obtained
May 1981	Ames, Iowa	F_1 plants were grown F_2 seeds were obtained	F_1 plants were grown BC_1F_1 seeds were obtained
Nov 1981	Puerto Rico		BC_1F_1 seeds were obtained
Feb 1982	Puerto Rico		BC_1F_2 seeds were obtained
May 1982	Ames, Iowa	F_2 plants were grown $F_{2:3}$ plants were obtained	BC_1F_2 plants were grown
May 1982	Puerto Rico		$BC_1F_{2:3}$ seeds were obtained
Nov 1982	Puerto Rico	$F_{2:3}$ lines were grown $F_{2:4}$ seeds were obtained	
Feb 1983	Puerto Rico	$F_{2:4}$ lines were grown $F_{4:5}$ seeds were obtained	$BC_1F_{2:3}$ lines were grown $BC_1F_{3:4}$ seeds were obtained
May 1983	Ames, Iowa	200 lines were planted 50 lines were selected	200 lines were planted 50 lines were selected
May 1984	Ames, Iowa	Yield Test	Yield test

BC_2	BC_3	BC_4
F_1 seeds were obtained	F_1 seeds were obtained	F_1 seeds were obtained
F_1 plants were grown BC_1F_1 seeds were obtained	F_1 plants were grown BC_1F_1 seeds were obtained	F_1 plants were grown BC_1F_1 seeds were obtained
BC_1F_1 seeds were grown BC_1F_1 seeds were obtained	BC_1F_1 seeds were grown BC_1F_1 seeds were obtained	BC_1F_1 seeds were grown BC_1F_1 seeds were obtained
BC_2F_1 plants were grown BC_2F_2 seeds were obtained	BC_2F_1 plants were grown BC_3F_1 seeds were obtained	BC_2F_1 plants were grown BC_3F_1 seeds were obtained
		BC_3F_1 plants were grown BC_4F_1 seeds were obtained
BC_2F_2 plants were grown $BC_2F_{2:3}$ seeds obtained	BC_3F_1 plants were grown BC_3F_2 seeds were obtained	
		BC_4F_1 plants were grown BC_4F_2 seeds were obtained
	BC_3F_2 plants were grown $BC_3F_{2:3}$ seeds were obtained	
200 lines were planted 50 lines were selected	200 lines were planted 50 lines were selected	BC_4F_2 plants were grown $BC_4F_{:3}$ seeds were obtained
Yield test	Yield test	Yield test

In May of 1983 at Ames, $F_{4:5}$, $BC_1F_{3:4}$, $BC_2F_{2:3}$ and $BC_3F_{2:3}$ lines were grown to select lines similar in phenotypic characteristics to the recurrent parents. Each set consisted on 110 entries, of which ten were the current parent. They were planted in hill plots for each generation of both the Cumberland and the A78-123018 cross. Twelve seeds per hill plot were planted. Ten seeds were saved for the phytophthora screening test. In July and August, the phytophthora screening test was conducted in the greenhouse to identify lines homozygous resistant to the pathogen. The procedure for determining the presence of $\underline{Rps}_1^k$ allele are described below.

Ten seeds from each line were planted in 10cm clay pots in the greenhouse. The check cultivars, Clark, Clark 63 and BSR 201 were also planted to determine the effectiveness of the test. Eight days after seeding, the plants were inoculated with mycelia of the pathogen from the cultured media. Inoculation was done by cutting a 1 cm slit in the stem below the cotyledonary node. A small piece of mycelia was inserted into the slit of the stem. Four days after, the plants were inoculated, scores were recorded based on how many plants have fallen over or rotted beyond the point of inoculation.

$$\text{Disease Score} = \frac{\text{No. of plants infected}}{\text{Total number of plants in a pot}}$$

To identify homozygous resistant plants, the following standards were used.

$\underline{Rps}_1^k$ $\underline{Rps}_1^k$ = 0/10, 0/9, or 1/10

$\underline{Rps}_1^k$ $\underline{rps}_1^k$ = 2/10 to 8/10

$\underline{rps}_1^k$ $\underline{rps}_1^k$ = 9/9, 9/10, or 10/10

Up to 50 lines of each were harvested from the field based on the following criteria:

1. Homozygous resistant to the disease based on the greenhouse screening test
2. Maturity within 3 days of the recurrent parent, and
3. Desirable for agronomic characteristics.

Selected lines were harvested individually in bulk.

For the BC_4F_2 generation at Ames, 153 lines of Cumberland and 164 lines of the A78-123018 crosses were planted in one set of 320 entries using one replication in one location. The entries were planted in short rows 75 cms long with 20 seeds per row. Maturity checks were planted as a border on both sides of each set. From each cross, 250 plants were harvested from rows segregating for resistance to phytophthora rot. The plants had a maturity within 3 days of their recurrent parent and were phenotypically similar to their recurrent parent.

In the winter of 1983 at Ames, the $BC_4F_{2:3}$ seeds were screened for phytophthora resistance using race 1 of the pathogen. The plants that were homozygous for $\underline{Rps}_1^k$ were entered in the 1984 yield test.

In the summer of 1984, lines representing the different generations were evaluated for yield and other agronomic characteristics (Table 5). Each set consisted of 260 entries; 50 entries for each of 5 generations, 5 check cultivars, and 5 replicates of the recurrent parent. The entries from each cross were grown in a randomized complete-block design with two replications at each of two locations. Twelve seeds per entry were planted in hill plots spaced 1 m apart. Entries from the crosses involving A78-123018 were evaluated at Ames and Corwith, and entries from the Cumberland crosses were evaluated at Ames and Stuart. The tests were planted on 12 May at Ames, 15 May at Stuart, and 16 May at Corwith.

The data were collected for seed yield and maturity. Seed yield was expressed in grams per square meter ($g\ m^{-2}$). Maturity was the date when 95% of the pods were mature, expressed as number of days after August 31.

Analyses of variance were performed for seed yield and maturity. All entries, except the check cultivars, were included in the analysis. Statistical analyses were conducted for individual locations an combined across locations. In this study, locations were assumed to be a random effect and generations were considered a fixed effect. For maturity, lines were regarded as a fixed effect because the plants from which they were derived were selected for this trait. For seed yield, lines were regarded as a random effect because there was no attempt made to select plants on the basis of yield.

For the analyses of data at each environment, the following statistical model was used:

Table 5. Number of lines evaluated from each generation

Cross	Generation	No. of lines
A78-123018	BC_0	50
	BC_1	50
	BC_2	50
	BC_3	50
	BC_4	50
Cumberland	BC_0	50
	BC_1	49
	BC_2	50
	BC_3	49
	BC_4	50

$$Y_{ij} = u + R_i + L_j + e_{ij}$$

where

Y_{ij} = overall value of the j^{th} line in the i^{th} replication

u = overall mean effect

R_i = effect of the i^{th} replication, i = 1 to 2

L_j = effect of the j^{th} line, j = 1 to 255 in the A78-123018 cross
1 to 253 in the Cumberland cross

The following model was used for the analyses of data combined across environments:

$$Y_{ijk} = u + E_i + R_{ij} + L_k + (ER)_{ik} + e_{ijk}$$

Where

Y_{ijk} = observed value for the k^{th} line in the j^{th} replication of the i^{th} location

u = overall mean effect

E_i = effect of the i^{th} location, i = 1 to 2

R_{ij} = effect of the j^{th} replication in the i^{th} location, j = 1 to 2

L_k = effect of the k^{th} line, k = 1 to 255 in the A78-123018 cross
1 to 253 in the Cumberland cross

$(ER)_{ik}$ = interaction effect between the i^{th} location and the k^{th} line

e_{ijk} = error associated with the ijk^{th} observation

For each analysis of variance, the mean squares due to lines were partitioned into two components: variation among lines within

generations and variation among generations. The mean squares due to lines within generations were further subdivided into six components: 1) among lines within the BC_0, 2) among lines with the BC_1, 3) among lines within BC_2, 4) among lines within BC_3, 5) among lines within BC_4, and 6) within the recurrent parent.

L.S.D. values for yield having significant values in the analysis of variance were calculated for data at individual locations and combined across locations. For comparing means of different generations, the L.S.D. values were calculated using the equation

$$\text{L.S.D.} = t_{df,\ 0.05} \sqrt{\text{EMS}\ (1/G_h + 1/G_p)}$$

where

EMS = error means square,

G_h = number of values used in computing means in generation h, and

G_f = number of values used in computing means in generation f.

For comparing means of various generations to recurrent parent means, the L.S.D. value was calculated using the equation

$$\text{L.S.D.} = t_{df,\ 0.05} \sqrt{\text{EMS}\ (1/G_n + 1/G_p)}$$

where

EMS = error means square,

G_n = number of values used in computing generation means, and

G_p = number of values used in computing recurrent parent means.

From the analyses of data at individual locations, the significance of lines and related components were tested against the error mean square (Table 6). For data combined across locations, the significance of lines was tested against the location x line mean square. The lines within each different generations were tested against their respective location x entry mean square unless the interaction was not significant, then the error means square was used to test their significance (Table 7).

Estimates of genetic variance (σ^2_g) were computed for yield using the formula:

$$\sigma^2_g = \frac{\text{(Entry mean square)} - \text{(Location x Entry mean square)}}{\text{(No. of replications)} \times \text{(No. of locations)}}$$

Table 6. Form of the analysis of variance for data from lines in different generations and the recurrent parent at individual locations with fixed and random line effects

Source of Variation	df[a]	Expected mean squares	
		Lines fixed	Lines random
Replications	(r-1)	$\sigma^2e + L\sigma^2r$	$\sigma^2e + L\sigma^2r$
Lines (L)	(l-1)	$\sigma^2e + RL^2$	$\sigma^2e + R\sigma^2_l$
L/Generation	(l-g)	$\sigma^2e(l/g) + R(L/G)^2$	$\sigma^2e(l/g) + R\sigma^2_{(l/g)}$
L in BC_0	(l_0-1)	$\sigma^2_e(0) + RL^2_0$	$\sigma^2_e(0) + R\sigma^2_l(0)$
L in BC_1	(l_1-1)	$\sigma^2_e(1) + RL^2_1$	$\sigma^2_e(1) + R\sigma^2_l(1)$
L in BC_2	(l_2-1)	$\sigma^2_e(2) + RL^2_2$	$\sigma^2_e(2) + R\sigma^2_l(2)$
L in BC_3	(l_3-1)	$\sigma^2_e(3) + RL^2_3$	$\sigma^2_e(3) + R\sigma^2_l(3)$
L in BC_4	(l_4-1)	$\sigma^2_e(4) + RL^2_4$	$\sigma^2_e(4) + R\sigma^2_l(4)$
Parent	(l_4-1)	$\sigma^2_e(p) + RL^2_4$	$\sigma^2_e(p) + R\sigma^2_l(p)$
Generation	(G-1)	$\sigma^2e(g) + RG^2$	$\sigma^2e(g) + R\sigma^2_g$
Error	(r-1)(l-1)	σ^2e	σ^2e

[a] R = replications, L = lines, and G = generations.

Table 7. Form of the analysis of variance for data from lines in different generations and the recurrent parent combined across locations

Source of Variation	df[a]	Expected mean squares	
		Lines fixed	Lines random
Locations (E)	(e-1)	$\sigma^2x + R\sigma^2_e$	$\sigma^2x + R\sigma^2_e$
Replications/E	e(r-1)	σ^2x	σ^2x
Lines (L)	(l-1)	$\sigma^2y + R\sigma^2 + REL^2$	$\sigma^2y + R\sigma^2_{le} + RE\sigma^2_l$
L/Generation(G)	(l-g)	$\sigma^2y(g/l)+R\sigma^2l/ge+RE(L/G)^2$	$\sigma^2y(g/l)+R\sigma^2l/ge + RE\sigma^2(L/G)$
L in BC_0	(l_0-1)	$\sigma^2_y(0) + R\sigma^2l(0)e+REL_0\sigma^2$	$\sigma^2y(0) + R\sigma^2_1(0)e + RE\sigma^2l(0)$
L in BC_1	(l_1-1)	$\sigma^2_y(1) + R\sigma^2l(1)e+REL^2_1$	$\sigma^2y(1)+R\sigma^2_1(1)e + RE\sigma^2l(1)$
L in BC_2	(l_2-1)	$\sigma^2_y(2) + R\sigma^2l(2)e+REL^2_2$	$\sigma^2y(2)+R\sigma^2_1(2)e + RE\sigma^2_1(2)$
L in BC_3	(l_3-1)	$\sigma^2_y(3) + R\sigma^2l(3)e + REL^2_3$	$\sigma^2y(3) + R\sigma^2_1(3) + RE\sigma^2l(3)$
L in BC_4	(l_4-1)	$\sigma^2_y(4) + R\sigma^2l(4)e + REL^2_4$	$\sigma^2_y(4) + R\sigma^2_1(4)e + RE\sigma^2l(4)$
Parent	(l_p-1)	$\sigma^2_y(4) + R\sigma^2l(p)e + RELp^2$	$\sigma^2_y(p) + R\sigma^2_1(p)e + RE\sigma^2l(p)$
Generation	(g-1)	$\sigma^2y(g) + R\sigma^2ge + REG^2$	$\sigma^2y(g) + R\sigma^2ge + REG^2_g$

E x L	(e-1)(1-1)	$\sigma^2 y + R\sigma^2 le$	$\sigma^2 y + R\sigma^2 le$
E x LG	(e-1)(1-g)	$\sigma^2 y(1/g) + R\sigma^2 1/ge$	$\sigma^2 y(1/g) + R\sigma^2 1/ge$
E x L in BC_0	(e-1)(1_0-1)	$\sigma^2 y(0) + R\sigma^2 1(0)e$	$\sigma^2 y(0) + R\sigma^2 1(0)e$
E x L in BC_1	(e-1)(1_1-1)	$\sigma^2 y(1) + R\sigma^2 1(1)e$	$\sigma^2 y(1) + R\sigma^2 1(1)e$
E x L in BC_2	(e-1)(1_2-1)	$\sigma^2 y(2) + R\sigma^2 1(2)e$	$\sigma^2 y(2) + R\sigma^2 1(2)e$
E x L in BC_3	(e-1)(1_3-1)	$\sigma^2 y(3) + R\sigma^2 1(3)e$	$\sigma^2 y(3) + R\sigma^2 1(3)e$
E x L in BC_4	(e-1)(1_4-1)	$\sigma^2 y(4) + R\sigma^2 1(4)e$	$\sigma 2y(4) + R\sigma^2 1(4)e$
E x Parent	(e-1)(1p-1)	$\sigma^2 y(p) + R\sigma^2 1(p)e$	$\sigma^2 y(p) + R\sigma^2 1(p)e$
E x G	(e-1)(g-1)	$\sigma^2 y(g) + R\sigma^2 ge$	$\sigma^2 y(g) + R\sigma^2 ge$
Error	e(r-1)(1-1)	$\sigma^2 y$	$\sigma^2 y$

[a]R=replications, L=lines, and G=generations.

RESULTS

Analyses of variance for each location in 1984 indicated significant differences for yield and maturity of the A78-123018 cross (Table 8). For the Cumberland cross, significant differences for yield and maturity were observed except for yield of Cumberland cross at Ames (Table 9). Variations among generations and lines within generations were partitioned from the variation among all lines. Highly significant differences were observed among generation at each location for yield and maturity of the A78-123018 cross. For the Cumberland cross, generations were significant at each location for maturity, while for yield, generation was significant only at Stuart.

For the combined analyses cross locations, highly significant differences were detected among lines for yield and maturity in both crosses (Tables 10 and 11). Significant variations were observed among generations for yield and maturity in both crosses. For lines within generation, lines within the BC_1 and BC_4 generation were significantly different for yield and maturity in the A78-123018 cross. Lines within the BC_0, BC_2, and BC_3 of the A78-123018 cross did not differ significantly for yield, but were significantly different for maturity. For the Cumberland cross, lines within backcross generations did not differ significantly for yield, except in BC_1. For maturity, there were significant differences among lines in each generation.

Significant differences were observed among locations for yield and maturity in both the A78-123018 cross and Cumberland cross (Table 10 and 11). The variation attributed due to locations may be due to differences

Table 8. Analyses of variance for yield and maturity of lines derived from the A78-123018 cross at individual locations in 1984

Sources of variation	df	Mean Squares			
		Ames		Corwith	
		Yield	Maturity	Yield	Maturity
Replications	1	114,046.08**	26.84**	2771.07**	76.10**
Lines (L)	254	1,648.77**	10.57**	504.96*	6.09**
L/Generations	249	1,232.51**	8.68**	440.74	4.55**
L in F_4	49	1,280.01	12.04**	343.69	7.34**
L in BC_1F_2	49	1,459.07**	7.27**	416.77	4.30**
L in BC_2F_2	49	1,188.43	8.18**	444.79	3.57**
L in BC_3F_2	49	1,027.67	9.33**	494.39	4.13**
L in BC_4F_2	49	1,215.71	7.26**	498.54	3.65**
A78-123018	4	1,129.59	0.50	508.06*	1.75
Generations	5	22,378.71**	104.74**	3703.30**	82.64**
Error	254	848.46	1.93	390.19	1.58
C.V.(%)		11.2	13.1	14.4	7.0

**Significant at the 0.05 and 0.01 probability levels, respectively.

Table 9. Analyses of variance for yield and maturity of lines derived from the Cumberland cross at individual locations in 1984

Sources of variation	df	Mean Squares			
		Ames		Corwith	
		Yield	Maturity	Yield	Maturity
Replications	1	38,696.89**	17.09**	12.49	0.05
Lines (L)	252	1,140.27	2.17**	431.58**	2.87**
L/Generations	247	1,125.74	2.00**	382.54*	2.61**
L in F_4	49	1,077.83	2.48**	245.67	2.44**
L in BC_1F_2	49	1,722.47**	2.02	554.60	3.53
L in BC_2F_2	49	907.70	1.92**	437.17*	2.37**
L in BC_3F_2	49	750.60	1.38*	364.07	2.14**
L in BC_4F_2	49	1,178.40	2.32**	344.12	2.73**
Cumberland	4	1,079.38	0.35	20.46	0.65
Generations	5	1,858.28	10.66**	2851.87**	15.67**
Error	252	1,001.46	0.99	296.75	0.92
C.V.(%)		14.0	4.4	7.5	4.4

*,**Significant at the 0.05 and 0.01 probability levels, respectively.

Table 10. Analysis of variance for yield and maturity of lines derived from the A78-123018 cross combined across locations in 1984

Sources of variation	df	Mean squares	
		Yield	Maturity
Locations (E)	1	3,835,823.56**	13,713.33**
Replications (R)/E	2	58,408.58**	51.47**
Lines (L)	254	1,372.46**	14.30**
L/Generations (L/G)	249	967.31**	10.91**
L in BC_0	49	928.69	17.06**
L in BC_1F_2	49	1,168.29*	9.84**
L in BC_2F_2	49	727.45	8.91**
L in BC_3F_2	49	905.88	10.72**
L in BC_4F_2	49	1,125.52**	8.80**
Parent	4	731.39	1.12
Generations (G)	5	21,584.60**	183.44**
E x L	254	781.28*	2.36**
E x L/G	249	705.93	2.33**
E x L in BC_0	49	695.07	2.32
E x L in BC_1F_2	49	707.55	1.73
E x L in BC_2F_2	49	905.78	2.84
E x L in BC_3F_2	49	616.18	2.73
E x L in BC_4F_2	49	588.73	2.10
E x Parent	4	906.26	1.12
E x G	5	4533.41**	3.95*
Error	508	619.32	1.75
C.V.(%)		12.5	9.2

*,**Significant at the 0.05 and 0.01 probability levels, respectively.

Table 11. Analysis of variance for yield and maturity of lines from the Cumberland cross combined across locations in 1984

Sources of variation	df	Mean squares	
		Yield	Maturity
Locations (E)	1	3,239.04*	184.41**
Replications (R)/E	2	19,354.69**	8.57**
Lines (L)	252	972.18**	3.98**
L/Generations (L/G)	247	915.26**	3.54**
L in BC_0	49	756.19	3.98**
L in BC_1F_2	48	1,566.90**	4.17**
L in BC_2F_2	49	766.51	3.22**
L in BC_3F_2	48	646.14	2.49**
L in BC_4F_2	49	874.95	4.07**
Parent	4	589.26	0.58
Generations	5	3,784.30**	25.65**
E x L	252	599.26	1.06
E x L/G	247	593.07	1.07
E x L in BC_0	49	567.31	0.97
E x L in BC_1F_2	48	710.16	1.38
E x L in BC_2F_2	49	578.37	1.06
E x L in BC_3F_2	48	468.52	1.04
E x L in BC_4F_2	49	647.58	0.97
E x Parent	4	510.58	0.42
E x G	5	925.84	0.69
Error	504	619.11	0.96
C.V.(%)		11.2	4.4

*,**Significant at the 0.05 and 0.01 probability levels, respectively.

in soil types and environmental conditions at the locations. Location differences were obvious in the A78-123018 cross (Table 12). The mean yield of all lines in the A78-123018 cross was 259 g m^{-2} at Ames and 137 g m^2 at Corwith. Therefore, it is likely that the combination of soil type and prevailing climatic condition may have contributed to the observed yield differences for these data. Maturity differences on the other hand are believed to be influenced primarily by its geographic location. Differences between locations in the Cumberland cross were less pronounced than in the A78-123018 cross. It is possible that the climatic and soil conditions used for evaluation in the Cumberland cross were more similar than in the A78-123018 cross.

There were significant differences for the line x location interaction in A78-123018 cross for yield and maturity. On the other hand, no significant line x location interactions were observed in the Cumberland cross for yield and maturity.

The coefficients of variation for yield and maturity were generally higher in the A78-123018 cross than in the Cumberland cross (Tables 7, 8, 9, and 10). This may be attributed to large deviations in yield and maturity at Ames from Corwith for the A78-123018 cross. In general, the coefficients of variation for yield were larger than for maturity.

For the A78-123018 cross at Ames, the mean yields of all generations were not significantly different from the mean yield of the recurrent parent (Table 12). Only mean yields of the BC_0 and BC_1 generations differed significantly from the mean yields of the BC_2, BC_3, and BC_4 generations. At Corwith, the mean yield averaged across all generations

Table 12. Mean performance of five generations from the A78-123018 cross and of the recurrent parent at individual locations in 1984

Generation	Ames		Corwith	
	Yield	Maturity	Yield	Maturity
	($g\ m^{-2}$)	days	($g\ m^{-2}$)	days
F4	238	10	128	17
BC_1F_2	244	9	133	17
BC_2F_2	269	11	138	18
BC_3F_2	271	12	139	19
BC_4F_2	273	11	145	19
A78-123018	261	10	136	18
$L.S.D._{0.05}$ (between BC_n)	12		8	
$L.S.D._{0.05}$ (BC_n vs A78-123018)	27		18	

Table 13. Mean performance of five generations from the Cumberland cross of the recurrent at individual locations in 1984

GENERATION	Ames		Corwith	
	Yield	Maturity	Yield	Maturity
	($g\ m^{-2}$)	days	($g\ m^{-2}$)	days
BC_0	220	23	222	22
BC_1F_2	223	23	223	22
BC_2F_2	232	23	231	22
BC_3F_2	228	22	235	21
BC_4F_2	223	23	233	22
Cumberland	230	22	233	21
L.S.D.$_{0.05}$ (between BC_n)	12		7	
L.S.D.$_{0.05}$ (BC_n vs Cumberland)	29		16	

did not differ significantly from the mean yield of the recurrent parent. Mean yields of BC_2, BC_3 and BC_4 generations differed significantly from the mean yields of BC_0 and BC_1 generation. The mean yields combined across locations showed similar trends to the results observed at each location (Table 14). The mean yield averaged across all generations did not differ significantly from the mean yield of Vinton 81. The mean yields the BC_0 and BC_1 generations differed significantly from the mean yields of the BC_2, BC_3, and BC_4 generations. For maturity, means of the different generation were either a day earlier or a day later in comparison with recurrent parent.

Table 14. Mean performance of five generations from the A78-123018 cross and of the recurrent parent across locations

Generation	% A78-123018 Germplasm	Trait	
		Yield	Maturity
		($g\ m^{-2}$)	(days)
BC_0	50.0	183 (92)[a]	13
BC_1F_2	75.0	189 (95)	13
BC_2F_2	87.5	204 (103)	15
BC_3F_2	93.8	206 (104)	15
BC_4F_2	96.9	209 (106)	15
A78-123018	100.0	198	14
L.S.D.$_{0.05}$ (between BC_n)		7	
L.S.D.$_{0.05}$ (BC_n vs A78-123018)		16	

[a]Numbers in parentheses are yield expressed as a percentage of the mean yield of A78-123018.

Table 15. Mean performance of five generations from the Cumberland cross of the recurrent parent across locations

Generation	% A78-123018 Germplasm	Trait	
		Yield	Maturity
		($g\ m^{-2}$)	(days)
BC_0	50.0	221 (96)[a]	23
BC_1F_2	75.0	223 (97)	22
BC_2F_2	87.5	231 (100)	22
BC_3F_2	93.8	232 (100)	22
BC_4F_2	96.9	229 (99)	22
Cumberland	100.0	231	21
$L.S.D._{0.05}$ (between BC_n)		7	
$L.S.D._{0.05}$ (BC_n vs Cumberland)		17	

[a]Numbers in parentheses are yield expressed as a percentage of the mean yield of Cumberland.

For the Cumberland cross. the mean yields of the generations did not differ significantly from the mean yield of the recurrent parent (Table 13). The mean maturity dates of the different generations were either a day earlier of later than the recurrent parent. When data were combined across locations, only the mean yields of the BC_0 and BC_1 generations differed significantly from the mean yield of the recurrent parent (Table 15).

One of the main concerns for a plant breeder is to know how much yield increase will be made for each backcross to the susceptible recurrent parent. Data obtained from this study revealed that comparable

mean yield to the recurrent parent could be obtained by the BC_2 generation in both crosses. Significant yield increases were observed up to the BC_2 generation, and from that generation, the increase in yield produced from each additional backcross was small (Fig. 1).

The frequency distributions of lines with yields better, equal or worse than the recurrent parent for the two crosses averaged across locations are presented in Table 16. The results indicated that in both crosses, a high percentage of the lines gave similar yields to the recurrent parent and only a small proportion had significantly poorer yields than the recurrent parent. For the A78-123018 cross, 94% of the liens in the BC_0 generation were similar in yield to the recurrent parent, and 90% of the lines of the BC_1 Generation were not significantly different in yield from the recurrent parent. All the lines in the BC_2, BC_3, and BC_4 generations either did not differ significantly from the recurrent parent or they exceeded the yield of the recurrent parent. Five lines in the BC_4 gave significantly higher yield than the A78-123018. For the Cumberland cross, 90% of the BC_0 lines were not significantly different in yield than the recurrent parent, and 92% of the BC_1 lines were equal in yield to the recurrent parent. Yields of all lines in the BC_2 and BC_3, and all but one line in the BC_4 did not differ significantly from the yield of Cumberland.

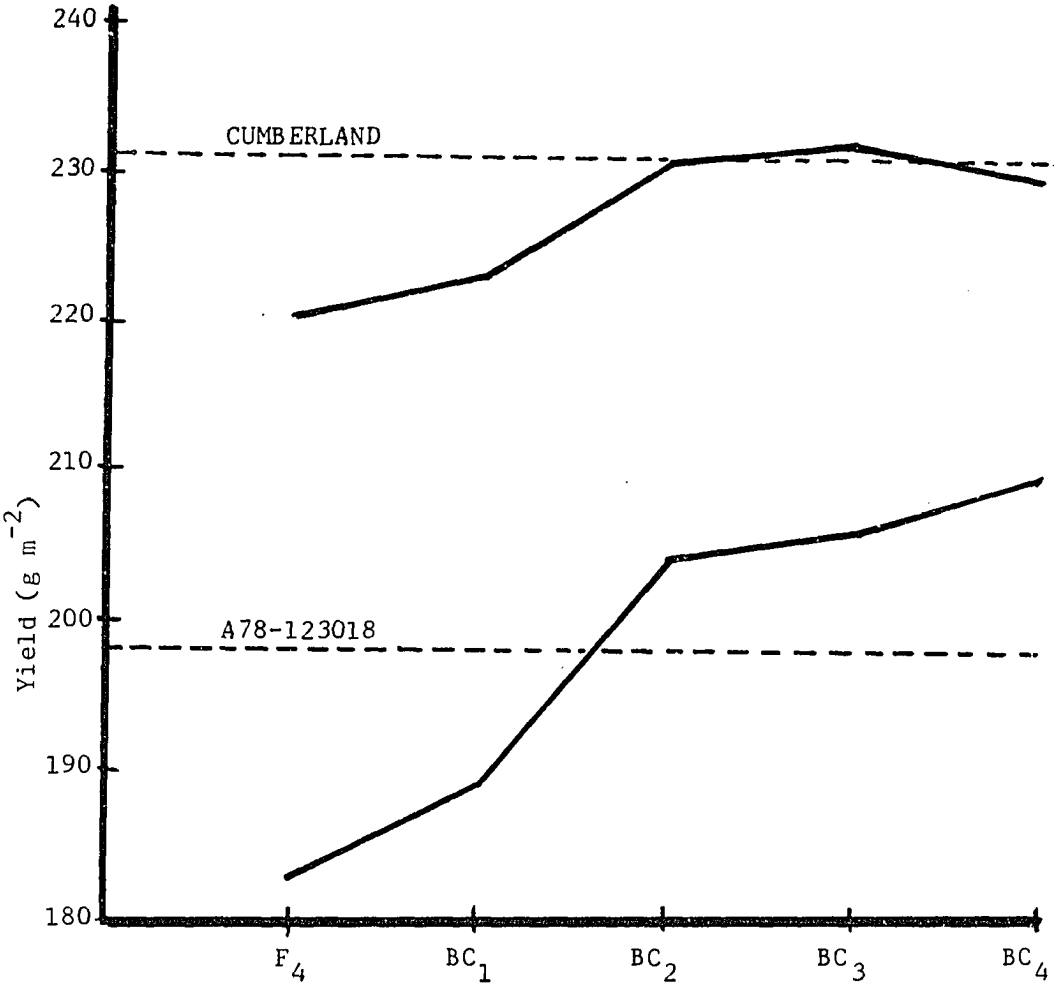

Fig. 1. Mean yield of each backcross generation versus the number of backcross generations

Table 16. Frequency distribution of lines better, equal, or worse than the recurrent parent for two crosses averages across two locations[a]

Cross	Generation				
	BC_0	BC_1	BC_2	BC_3	BC_4
A78-123018					
Better	0	0	1	0	5
Equal	47	45	49	50	45
Worse	3	5	0	0	0
Cumberland					
Better	0	0	0	0	0
Equal	49	45	50	49	49
Worse	1	4	0	0	1

[a]Comparisons based on L.S.D. value at 0.05 level of probability.

The estimates of genetic variance for yield of the Cumberland cross showed that the highest genetic variance was produced in the BC_1 generation (Table 17). The genetic variance decreased in BC_2 and remained at a relatively constant level in the BC_3 and BC_4. On the other hand, the genetic variance for yield of the different generations of the A78-123018 cross did not show a consistent trend. A negative genetic variance estimate was obtained in the BC_2 generation, while higher genetic variance were observed in the BC_1 and BC_4 generations than in the other generations.

Table 17. Estimates of genetic variance for yield of five generations from two soybean crosses in 1984

Cross	BC_0	BC_1	BC_2	BC_3	BC_4
A78-123018	58.4±57.4	115.2±167.6	-44.6±57.5	72.4±54.2	134.2±62.9
Cumberland	47.2±46.8	214.2±86.0	47.0±47.5	44.4±39.9	56.8±53.9

DISCUSSION

The main goal of backcrossing is to recover the characteristics of the recurrent parent, except for the character being transferred from the donor parent. In breeding for resistance to phytophthora rot, the primary concern is to recover the yield potential of the recurrent parent and acquire the resistance gene(s) from the donor parent. In this study, satisfactory recovery of yield was obtained in the BC_2 and succeeding generations for both crosses. Selection for lines with the same maturity as the recurrent parent seemed to present no problem because the mean values of the different backcross generations varied only 1 or 2 days from the recurrent parent in both crosses.

The estimates of genetic variance from both crosses showed relatively high genetic variance beginning in the BC_1 generation. Also, considerable genetic variation was shown in the BC_4 generation of A78-123018. It was at the BC_4 generation that five transgressive segregates were observed. It is possible that continued segregation of genes for yield may have occurred in the BC_4 generation. Wilcox et al. (1971) observed some deviation from predicted performance and cited continued segregation even in the BC_4 to BC_7 generation as one of the possible explanations. In a study of individual F_3 plant progenies in a soybean cross, Mahmud and Kramer (1951) calculated that the last generation in which significant differences among soybean lines could be expected would be in F_6 for yield. Because the return to homozygosity with selfing is at the same rate with backcrossing, continued segregation observed in the BC_4 closely agrees with data reported by Wilcox et al.

(1971) and Mahmud and Kramer (1951).

It is evident from this study that the chance of recovering lines with comparable yield to the recurrent parent is high. However, the probability of obtaining transgressive segregates for yield seems to be very low. In A78-123018, only five transgressive segregates were observed out of 50 lines in the BC_4 generation tested at two locations. This represents only 2 % among all the lines tested. These lines were considered transgressive segregates because they gave significantly higher yields than the recurrent parent, A78-123018, at the 5 % probability level. At this probability level, 2.5 % of the lines are expected to yield greater than the recurrent parent by chance. It is possible that these segregants were not in reality higher yielding than A78-123018. Further testing of these lines is recommended to verify whether the increase in yield was actually due to genotypic effects or due to chance events.

Data from this study indicated the possibility of compositing visually similar lines derived from the BC_2 generation. The mean values for yield and maturity and the high frequency of lines showing similar yield to the recurrent parent in the BC_2 generation both strongly support this contention. Furthermore, mean yields of lines derived from the BC_2 generation in both crosses did not significantly vary from the succeeding backcross generations. The results obtained in this study did not substantiate the conclusion of Wilcox et al. (1971) that seven backcrosses would be desirable for transferring a gene for phytophthora rot resistance into susceptible cultivars. Two instead of

seven backcrosses were found sufficient to find resistant lines with yield similar to the recurrent parent. The difference in results may be attributed to differences in the performance of the donor parents. In my study, the differences in yield between the recurrent parent and donor parents were not high, whereas in the study of Wilcox et al. (1971), each of the recurrent parents yielded 400 to 600 kg/ha more than the donor parent (Mukden). This exhibited the critical role donor parents can have in the performance of lines derived from backcrosses.

The results from this study indicated that with the use of good donor parents, the number of backcrosses required to composite similar lines without yield testing would be reduced from seven (Wilcox et al., 1971) to only two. When a satisfactory donor parent is used, advanced stages of backcrossing may not be essential if the sole purpose is to recover lines with similar yield, maturity and other agronomic characteristics. The results also indicated that it should be acceptable to bulk a group of visually similar lines from the third or later generations of backcrossing. With a low proportion of desirable transgressive segregates, it does not seem logical to perform further backcrossing after the BC_2 generation.

SUMMARY AND CONCLUSION

Crosses were made to transfer a gene for resistance to Phytophthora megasperma Drecks. var. sojae Hildeb. from Williams 82 into two susceptible genotypes, Cumberland, a high-yielding cultivar, and A78-123018, a high-yielding experimental line. Four backcrosses to each of the recurrent parents were made. The populations were used to determine the number of backcross generations required to transfer a major gene for phytophthora rot resistance into a cultivar and obtain lines with the yield potential of the recurrent parent and to determine in what backcross generation a composite of visually similar lines could be made that would yield as much as the recurrent parent.

In the summer of 1984, lines comprising the BC_0, BC_1, BC_2, BC_3, and BC_4 generations were evaluated for yield and maturity. The entries from each cross were grown in a randomized complete-block design with two replications at each of two Iowa locations. Entries from the crosses involving A78-123018 were evaluated at Ames and Corwith, whereas entries from the Cumberland cross were evaluated at Ames and Stuart.

Significant differences for yield and maturity were observed among lines derived from the different backcross generations. Highly significant differences were observed among generations for yield and maturity in both crosses. Lines within generations were not statistically significant for yield, in most of the generations, but significant differences were observed for maturity.

Results from this study revealed that on the average for the two crosses, 92 % of the lines in the BC_0 had similar yields to the recurrent

parent while about 91 % of the lines in the BC_1 generation have yields that did not significantly differ from the recurrent parent. In succeeding backcross generations after BC_1, yields of all lines (except one line in BC_4 of Cumberland) either did not significantly differ from the recurrent parent or they exceeded the yield of the recurrent parent.

These results have some important implications in backcross breeding for Phytophthora resistance in soybeans. They indicate that BC_2-derived lines phenotypically similar to the recurrent parent and with homozygous resistance to the pathogen can be composited without the need of evaluating for yield and other agronomic characteristics. Two backcrosses were found to be the most effective method of transferring a gene for phytophthora rot resistance into susceptible soybean lines or cultivars.

GENERAL CONCLUSION

In breeding for high-protein cultivars of soybean, it was found that the single-cross method was slightly superior in the identification of high-yielding lines with high protein percentage. Two lines from the F_4 generation were found that had significantly greater yield and equal protein percentage to Vinton 81.

In transferring Phytophtyora resistance in soybean by backcrossing, results showed that almost 100 % of the lines from the BC_2 and succeeding generations had comparable yields to the recurrent parent. It was concluded that two backcross would be the most effective method of transferring a gene for Phytophthora rot resistance into susceptible cultivars.

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